

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:15:49 : Search time 172.18 Seconds
(without alignments)
472.225 Million cell updates/sec

Title: US-09-052-089a-2
Perfect score: 2393
Sequence: 1 MPILSLCTICSDPFHSDV.....VRKTVSSASQPKIDFLCQ 470

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp._archaea:*
2: sp._bacteria:*
3: sp._fungi:*
4: sp._human:*
5: sp._invertebrate:*
6: sp._mammal:*
7: sp._mhc:*
8: sp._organelle:*
9: sp._phage:*
10: sp._plant:*
11: sp._rodent:*
12: sp._virus:*
13: sp._vertebrate:*
14: sp._unclassified:*
15: sp._virus:*
16: sp._bacteriophage:*
17: sp._archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	2315	96.7	470	11 008854	008854 mus musculus
2	2306	96.4	470	11 09CP4	09CP4 mus musculus
3	1826.5	76.3	469	4 09BWF2	09BWF2 homo sapien
4	1798.5	75.2	469	4 000467	000467 homo sapien
5	1045	43.7	223	11 0922M8	0922M8 mus musculus
6	919	38.4	433	13 09G2M8	09G2M8 mus musculus
7	281.5	11.8	455	5 09V8D7	09V8D7 fuigu rubrip
8	280.5	11.7	435	5 09V8D7	09V8D7 drosophila
9	221	9.2	506	10 09M143	09M143 drosophila
10	204.5	8.5	425	5 P90990	P90990 caenorhabdi
11	204.5	8.5	2473	11 090284	090284 mus musculus
12	200.5	8.4	1690	5 044829	044829 drosophila
13	195.5	8.2	1690	5 09VTE5	09VTE5 drosophila
14	191.5	8.0	2139	5 007569	007569 entamoeba h
15	190	7.9	2017	5 094992	094992 drosophila
16	190	7.9	2056	5 09W0W8	09W0W8 drosophila

17	190	7.9	2057	5 094987	094987 drosophila
18	189.5	7.9	1447	11 090YR2	090YR2 mus musculus
19	189.5	7.9	1487	11 090YR3	090YR3 mus musculus
20	188.5	7.9	574	4 09H810	09H810 homo sapien
21	188.5	7.9	2138	5 09X2E3	09X2E3 amoeba prot
22	186.5	7.8	1156	17 028714	028714 archaeoglob
23	184	7.7	1941	5 026079	026079 placopecten
24	183.5	7.7	1937	13 091B04	091B04 gallus gall
25	183	7.6	1219	5 09N223	09N223 aequipecten
26	181.5	7.6	1871	5 09NCL3	09NCL3 drosophila
27	181	7.6	324	11 09EON8	09EON8 mus musculus
28	181	7.6	1156	16 066878	066878 aquifex aeo
29	181	7.6	1933	13 090337	090337 cyprinus ca
30	181	7.6	1940	5 09U7E3	09U7E3 pecten maxi
31	181	7.6	2007	13 002015	002015 gallus gall
32	180	7.5	692	5 096720	096720 dermatophag
33	180	7.5	1992	5 021440	021440 caenorhabdi
34	179.5	7.5	1709	4 09UPS8	09UPS8 homo sapien
35	179.5	7.5	1710	4 09H1Q1	09H1Q1 homo sapien
36	179	7.5	1092	13 090338	090338 cyprinus ca
37	179	7.5	1950	5 026080	026080 placopecten
38	178.5	7.5	471	4 09BNG0	09BNG0 homo sapien
39	178.5	7.5	1999	11 063731	063731 rattus norv
40	178	7.4	482	5 09VBD21	09VBD21 drosophila
41	178	7.4	555	5 0961U3	0961U3 drosophila
42	178	7.4	1229	5 09N122	09N122 aequipecten
43	178	7.4	1243	5 09N121	09N121 aequipecten
44	178	7.4	1253	5 09N120	09N120 aequipecten
45	178	7.4	1790	3 007380	007380 saccharomyc

ALIGNMENTS

RESULT 1
ID 008854 PRELIMINARY; PRT; 470 AA.
AC 008854:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MTRIP.
GN TRAP OR MTRIP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97258620; PubMed=9104814;
RA Lee S.Y., Lee S.Y., Choi Y.;
RT "TRAF-Interacting protein (TRIP): a novel component of the tumor
necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
that inhibits TRAF2-mediated NF-kappaB activation.";
RL J. Exp. Med. 185:1275-1285(1997).
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: U77844; AAB52994.1; -.
DR MGD; MGI:1096377; Trrip.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zfc3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 470 AA; 53191 MW; 00FD705B52645133 CRC64;

Query Match 96.7%; Score 2315; DB 11; Length 470;
Best Local Similarity 97.7%; Pred. No. 4e-116;
Matches 459; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 MPILSLCTICSDPFHSDVAHICGHTFLQCLIQWFTAPSRCTCPOCRIOVGKTTIN 60
DB 1 MPILSLCTICSDPFHSDVAHICGHTFLQCLIQWFTAPSRCTCPOCRIOVGKTTIN 60

QY 61 KLFDLAQEEENVDAEFLKNELDVSKAQLSOKREKRDQAIIIDTLTLDTEENAVTES 120
 DB 61 KLFDLAQEEENVDAEFLKNELDVSKAQLSOKREKRDQAIIIDTLTLDTEENAVTES 120
 QY 121 LQNALNKAEMICSTLKKOMKFLQRODETKQAREBAHRLCKMKMTQEOIELLOSQRSEV 180
 DB 121 LQNALNKAEMICSTLKKOMKFLQRODETKQAREBAHRLCKMKMTQEOIELLOSQRSEV 180
 QY 181 EEMLRDMGVGSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSRSKLTN 240
 DB 181 EEMLRDMGVGSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSRSKLTN 240
 QY 241 TELDQAKLELSAQKDLSADQDEITSLRKSSDPPGNLEPASATNETVSRVLFESPAPVE 300
 DB 241 TELDQAKLELSAQKDLSADQDEITSLRKSSDPPGNLEPASATNETVSRVLFESPAPVE 300
 QY 301 MMRRLHOPPPGDEIDLNTTFDVNTPTQTSQSOHCLPKKICLERANSPMONVLKVKHV 360
 DB 301 MMRRLHOPPPGDEIDLNTTFDVNTPTQTSQSOHCLPKKICLERANSPMONVLKVKHV 360
 QY 361 SKPESQSLSGQRCVGEDELGAFLFIRNAVVGQKQPKRTAESRSTDVVRIGFDG 420
 DB 361 SKPESQSLSGQRCVGEDELGAFLFIRNAVVGQKQPKRTAESRSTDVVRIGFDG 420
 QY 421 LGGRTKFIOPRDTTIIIRPVVSKAKSKOKVRITVSSASQPKLDITFLCQ 470
 DB 421 LGGRTKFIOPRDTTIIIRPVVSKAKSKOKVRITVSSASQPKLDITFLCQ 470

RESULT 2

Q9CP4 PRELIMINARY; PRT; 470 AA.

AC 09CP4: 01-JUN-2001 (TREMBLERL 17, Created)
 DT 01-JUN-2001 (TREMBLERL 17, Last sequence update)
 DE 01-DEC-2001 (TREMBLERL 19, Last annotation update)
 DE TRAF-INTERACTING PROTEIN.
 GN TRAF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; Pubmed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi S., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kodota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AK012948; BAB28567.1; -
 DR EMBL: AK012786; BAB28469.1; -
 DR MGD: MGI:1096377; Traip
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00184; RING; 1.

KW Zinc-finger.
 SQ SEQUENCE 470 AA; 53149 MW; EBFARCA9A9F4BF2E CRC64;

Query Match 96.4%; Score 2306; DB 11; Length 470;
 Best Local Similarity 97.2%; Pred. No. 1,2e-115;
 Matches 457; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 MPILSLCTICSDFFDHSRDVAIHGHTFHLQCLIQMFETAPSRPCQCRIVGKKITIN 60
 DB 1 MPILSLCTICSDFFDHSRDVAIHGHTFHLQCLIQMFETAPSRPCQCRIVGKKITIN 60
 QY 61 KLFDLAQEEENVDAEFLKNELDVSKAQLSOKREKRDQAIIIDTLTLDTEENAVTES 120
 DB 61 KLFDLAQEEENVDAEFLKNELDVSKAQLSOKREKRDQAIIIDTLTLDTEENAVTES 120
 QY 121 LQNALNKAEMICSTLKKOMKFLQRODETKQAREBAHRLCKMKMTQEOIELLOSQRSEV 180
 DB 121 LQNALNKAEMICSTLKKOMKFLQRODETKQAREBAHRLCKMKMTQEOIELLOSQRSEV 180
 QY 181 EEMLRDMGVGSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSRSKLTN 240
 DB 181 EEMLRDMGVGSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSRSKLTN 240
 QY 241 TELDQAKLELSAQKDLSADQDEITSLRKSSDPPGNLEPASATNETVSRVLFESPAPVE 300
 DB 241 TELDQAKLELSAQKDLSADQDEITSLRKSSDPPGNLEPASATNETVSRVLFESPAPVE 300
 QY 301 MMRRLHOPPPGDEIDLNTTFDVNTPTQTSQSOHCLPKKICLERANSPMONVLKVKHV 360
 DB 301 MMRRLHOPPPGDEIDLNTTFDVNTPTQTSQSOHCLPKKICLERANSPMONVLKVKHV 360
 QY 361 SKPESQSLSGQRCVGEDELGAFLFIRNAVVGQKQPKRTAESRSTDVVRIGFDG 420
 DB 361 SKPESQSLSGQRCVGEDELGAFLFIRNAVVGQKQPKRTAESRSTDVVRIGFDG 420
 QY 421 LGGRTKFIOPRDTTIIIRPVVSKAKSKOKVRITVSSASQPKLDITFLCQ 470
 DB 421 LGGRTKFIOPRDTTIIIRPVVSKAKSKOKVRITVSSASQPKLDITFLCQ 470

RESULT 3

Q9BWF2 PRELIMINARY; PRT; 469 AA.

AC 09BWF2: 01-JUN-2001 (TREMBLERL 17, Created)
 DT 01-JUN-2001 (TREMBLERL 17, Last sequence update)
 DE 01-DEC-2001 (TREMBLERL 19, Last annotation update)
 DE TRAF-INTERACTING PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG CARCINOMA;
 RA Straussberg R.;
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: BC000310; AAH00310.1; -
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 469 AA; 53294 MW; B9EF3808FBC5985B CRC64;

Query Match 76.3%; Score 1826.5; DB 4; Length 469;
 Best Local Similarity 77.6%; Pred. No. 4.3e-90;
 Matches 363; Conservative 41; Mismatches 63; Indels 1; Gaps 1;
 QY 1 MPILSLCTICSDFFDHSRDVAIHGHTFHLQCLIQMFETAPSRPCQCRIVGKKITIN 60
 DB 1 MPILSLCTICSDFFDHSRDVAIHGHTFHLQCLIQMFETAPSRPCQCRIVGKKITIN 60

Db	1	MPRALCTICSPFHSHSDVAIAHCGHFFHLOCLQIOWETAPSRKPCQCRIOYVKRTIIN	60
Qy	61	KLFEDLAEENEVLDAEFLKNELDVSQAOLSKDREKRDQAIIIDTLRDLTEERNATVES	120
Db	61	KLFEDLAEENEVLDAEFLKNELDVNRQAOLSKDREKRDQVLIIDTLRDLTEERNATVES	120
Qy	121	LQNALNKAEMLCSTLKKQMKFLEORHODTEKQAREAHRLKCKMKMTMEDTELLLOSRESEV	180
Db	121	LQNALNKAEMLCSTLKKQMKTYLQOQDTEKQAEARRLRSMKMTMEDTELLLOSOREV	180
Qy	181	EEMIRDMGVGSAVBQILAVYCVSLKEKEYENLKEARKATAGELADRLKDLVSSRSKLTLN	240
Db	181	EEMIRDMGVGSAVBQILAVYCVSLKEKEYENLKEARKASGEVADRLKDLVSSRSKLQIVY	240
Qy	241	TELQAKTELNSAQKDLOSADOEITSLKKSDPDPCGNLEPASATETYSRLVESPAYE	300
Db	241	SELQDAKTELNSAQKDLOSADKEITSLKKLTMLQETLNLPPVASETVDRVLESAPAYE	300
Qy	301	MMNPFLHAPPEGDEIDLWTTFEDVNTPPQTSQSHCLPKKLCLEBARSPMONTLKKVVKY	360
Db	301	VNKLRLRPSRFDIDLNATEDVDVDPAPRPSQSHGYIEKLCLEKSHSPIDQVPKCKICKG	359
Qy	361	SKPESQSLGGGRCVGEIDELAGAFPLFIRNAVIGQKQPNFTAESRSTDVIRIGFDG	420
Db	360	PKRESQSLGGGSCAGEDEELVGAFFLFRNALIGQKQKPRRSESSCKMYVRTGPDG	419
Qy	421	LGGRKFTLOPNDTIIIRVPVYKSKSKSKOKYIKVTSSASQPKLDTFL	468
Db	420	LGGRKFTLOPNDTVWIRPLPVKPKTKVQKRVAKVTIVSLFOAKLDTFL	467
RESULT	4		
000467			
ID	000467	PRELIMINARY;	PRT: 469 AA.
AC	000467;		
DT	01-JUL-1997	(TREMBLrel. 04, Created)	
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	HTRP.		
GN	HTRP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97258620; PubMed=9104814;		
RA	Lee S.Y., Lee S.Y., Choi Y.		
RT	"TRAF-Interacting protein (TRIP): a novel component of the tumor		
RT	necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes		
RT	that inhibits TRAF2-mediated NF-kappaB activation.";		
RL	J. Exp. Med. 185:1275-1285(1997).		
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
DR	EMBL; U77845; AAB52993.1; -		
DR	InterPro; IPR001841; Znf_ring.		
DR	Pfam; PF00097; 14f-C3HC4; 1.		
DR	SMART; SM00184; RING; 1.		
FM	Zinc-finger.		
QO	SEQUENCE 469 AA; 53138 MW; 2D54ED04B84ABA4 CRC64;		

Query Match	75.2%;	Score 1798.5;	DB 4;	Length 469;
Best Local Similarity	76.9%;	Pred. No. 1.3e-88;		
Matches 360;	Conservative 41;	Mismatches 66;	Indels 1;	Gaps 1;

QY	1	MP	S	L	I	C	T	S	D	E	F	D	H	S	R	D	N	A	I	H	G	G	T	H	L	O	C	I	O	M	E	F	A	P	S	R	T	C	O	C	I	O	V	G	K	T	I	N	60										
Db	1	MP	A	L	T	C	I	C	S	D	E	F <td>D</td> <td>H</td> <td>S</td> <td>R</td> <td>D</td> <td>N</td> <td>A</td> <td>I</td> <td>H</td> <td>G <td>G</td> <td>T</td> <td>H</td> <td>L</td> <td>O</td> <td>C</td> <td>I</td> <td>O</td> <td>M</td> <td>E</td> <td>F</td> <td>A</td> <td>P</td> <td>S</td> <td>R</td> <td>T</td> <td>C</td> <td>O</td> <td>C</td> <td>I</td> <td>O</td> <td>V</td> <td>G</td> <td>K</td> <td>T</td> <td>I</td> <td>N</td> <td>60</td> </td>	D	H	S	R	D	N	A	I	H	G <td>G</td> <td>T</td> <td>H</td> <td>L</td> <td>O</td> <td>C</td> <td>I</td> <td>O</td> <td>M</td> <td>E</td> <td>F</td> <td>A</td> <td>P</td> <td>S</td> <td>R</td> <td>T</td> <td>C</td> <td>O</td> <td>C</td> <td>I</td> <td>O</td> <td>V</td> <td>G</td> <td>K</td> <td>T</td> <td>I</td> <td>N</td> <td>60</td>	G	T	H	L	O	C	I	O	M	E	F	A	P	S	R	T	C	O	C	I	O	V	G	K	T	I	N	60									
QY	61	K	L	F	D	L	A	O	E	E	N	V	I	D	A	E	F	L	K	N	E	L	D	S	V	A	K	O	S	Q	K	R	E	K	R	D	R	E	K	R	D	S	O	A	I	I	D	L	R	D	L	E	R	N	A	T	V	S	120
QY	61	K	L	F	D	L	A	O	E	E	N	V	I	D	A	E	F	L	K	N	E	L	D	S	V	A	K	O	S	Q	K	R	E	K	R	D	R	E	K	R	D	S	O	A	I	I	D	L	R	D	L	E	R	N	A	T	V	S	120
QY	61	K	L	F	D	L	A	O	E	E	N	V	I	D	A	E	F	L	K	N	E	L	D	S	V	A	K	O	S	Q	K	R	E	K	R	D	R	E	K	R	D	S	O	A	I	I	D	L	R	D	L	E	R	N	A	T	V	S	120
QY	61	K	L	F	D	L	A	O	E	E	N	V	I	D	A	E	F	L	K	N	E	L	D	S	V	A	K	O	S	Q	K	R	E	K	R	D	R	E	K	R	D	S	O	A	I	I	D	L	R	D	L	E	R	N	A	T	V	S	120
QY	61	K	L	F	D	L	A	O	E	E	N	V	I	D	A	E	F	L	K	N	E	L	D	S	V	A	K	O	S	Q	K	R	E	K	R	D	R	E	K	R	D	S	O	A	I	I	D	L	R	D	L	E	R	N	A	T	V	S	120
QY	61	K	L	F	D	L	A	O	E	E	N	V	I	D	A	E	F	L	K	N	E	L	D	S	V	A	K	O	S	Q	K	R	E	K	R	D	R	E	K	R	D	S	O	A	I	I	D	L	R	D	L	E	R	N	A	T	V	S	120
QY	61	K	L	F	D	L	A	O	E	E	N	V	I	D	A	E	F	L	K	N	E	L	D	S	V	A	K	O	S	Q	K	R	E	K	R	D	R	E	K	R	D	S	O	A	I	I	D	L	R	D	L	E	R	N	A	T	V	S	120
QY	61	K	L	F	D	L	A	O	E	E	N	V	I	D	A	E	F	L	K	N	E	L	D	S	V	A	K	O	S	Q	K	R	E	K	R	D	R	E	K	R	D	S	O	A	I	I	D	L	R	D	L	E	R	N	A	T	V	S	120
QY	61	K	L	F	D	L	A	O	E	E	N	V	I	D	A	E	F	L	K	N	E	L	D	S	V	A	K	O	S	Q	K	R	E	K	R	D	R	E	K	R	D	S	O	A	I	I	D	L	R	D	L	E	R	N	A	T	V	S	120
QY	61	K	L	F	D	L	A	O	E	E																																																	

QY	121	LONALNKAEMLCSTLKKOMKFLERODETQOAREBAHRLCKCAKKTMDIOELLLOQSORSEY	180
Db	121	LOQALGKAKEMLCSTLKKOMKYLEOQOODETQOAOEEGRLSRKCKMTKEOIELLOQSOPEY	180
QY	181	EEMIRDMCVGGSAAVEQOLAAVYCVSLKKEYLEMKERRATGTGLARLKKDLVSSRSKTKTLN	240
Db	181	EEMIRDMCVGGSAAVEQOLAAVYCVSLKKEYLEMKERRAAGSVAQKLRKDLFSSRSKLTQTVY	240
QY	241	TELODAKLELBSAOKDLOSADOETLSLRRKSDPPGNLBPASATNENVSRLYESPAPVE	300
Db	241	SELDOAKLELBSAOKDLOSADKELMSLKKTLTMOETLNLPPVASETVDRVLYESAPAVE	300
QY	301	MMNPLRHOPPRGDEIDINTFTEDVTNPTQTOGSGOHLCKLCLTERASPQONLKKRKHVY	360
Db	301	VNKLRRRSPRRDIDLNATFVDVTFPPARSSOHHGYEKLCEKSHSPIQDVPKIKCG	359
QY	361	SKPESQSLGGORCVGBLDEELAGAPLFLTRNAVLGOKOPNRTTAESRSTDVYRTGFDG	420
Db	360	PKRESQSLGGOCSGAGEDEELVAGAPLFIWNALIGOKOPKRRSESSCKDVAVRGTGFDG	419
QY	421	LGGRKFKIQPRDITTLIRPVPKKSAKSKQAKVIRKTVBSAQPRLDTFL	468
Db	420	LGGRKFKIQPRDITVIMIRPLVPKPKTKKORAKRVATVSLQOALDTFL	467

RESULT	5
Q922M8	
ID	Q922M8
PRELIMINARY;	
PRT;	223 AA.

DT	01-DEC-2001 (TReMBLrel. 19, Created)
DT	01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)

05 Mus musculus (Mouse).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Mus.

RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
PT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases

DR EMBL: BC006929; AA06929.1; -.
SO SEQUENCE 223 AA; 2584 MW; 412291C205C43071 CRC64;

Query Match	43.7%;	Score 1045;	DB 11;	Length 223;
Best Local Similarity	99.0%;	Pred. No. 8.6e-49;		
Matches 204; Conservative	1;	Mismatches 1;	Indels 0;	Gaps

```

07 1 MFISDCLISDFEIDSRDVAHICHGTFHDLQIOWEIAFSKCPQCNQIVGKNILIN 80
    || : |||||
Db 1 MPIRALCTISDFEIDSRDVAHICHGTFHDLQIOWEIAFSKCPQCNQIVGKTIIN 60

```

61 KLPFLAQEEENVLDAEFLKNEFLDSVKAQLSQDKREKRSQALIDTLRDTLEERNATVES 120

```

121 LÖNLINKAEMICSTLTKÖMFELEQRODETKQAREEAHRLCKMKTMEQTELLLOSQSEV 180

```

Db 181 EEMIRDMGVGOSAVEQLAVYCVSLKK 206

RESULT	6
Q9YGN2	
ID	Q9YGN2
PRELIMINARY;	
PRT;	433 AA.

DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)


```

Db 183 ----EADPHVLAMVSTLKLRELROCESKKTLELRNVKVVQNDLKRKEIELKRAYHNIPNV 238
QY 242 -----ELDQAKLELRSA--QKDLQADQETSLRKS---DDPGNLEPASANEVSR 290
Db 239 FIIDMCSFDSCKLEERVSHLESPLYQAOEKLOAEKNTAYLDSP---NMSCGLNSILA 294
QY 291 LVEE-----SPAVEMANRLHQPFGDEIDLNTTFDVNTPPTQSGSQHCLPKK--LC 342
Db 295 LKREERTTISPYKENIK-----RIESTSPYLN-KSSVGLAHLNTKGNIG 343
QY 343 LERAR-SPMONLKKVHKVSKESPQSLGQRCVGELEDELAGAPLEFIRNAVLGOKOPN 401
Db 344 LAKSKIPIKGGVGGVSMTS-----GTRKTSDDLSEKYSIF-----KKPR 384
QY 402 RTTAESSRSIDVVRIG---FDGLGRTKFIQPRDTTIIIRVPVSKAKSKOKVRITVS 457
Db 385 LLGSSSSSALTATTGTFNFMGMGSEK-----VDPFAQRAEEGLSTIRSSAL 435
QY 458 S 458
Db 436 S 436

RESULT 8
Q95SS5 PRELIMINARY; PRT; 435 AA.
ID Q95SS5
AC Q95SS5;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE GH03577P.
GN CS5140.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Garlin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celisner S.;
RU Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY060610; AL28158.1; -.
SQ SEQUENCE 435 AA; 48455 MW; 0BFF0AC81DD9416E CRC64;

Query Match 11.7%; Score 280.5; DB 5; Length 435;
Best Local Similarity 22.0%; Pred. No. 9.3e-08;
Matches 104; Conservative 99; Mismatches 187; Indels 83; Gaps 17;

QY 7 CTTCSDFFDSRDVAALHCGHTFHLOCLIQWFEFAPSRTCPCRIQVQKTIINKLEFDL 66
Db 6 CVICALFEGADVEFAFVCGMHFNCLNQWDR--SKTCQCKNKCTTRNIF-RVFNFL 62
QY 67 AQEEENVLAEFLKNEIDSVYKAQLSQDKREKRSQAIITDLRLTEERNATVESIQNALN 126
Db 63 ANLDVSHIDVSGIQEQLDNLMSKMYEKERNKDEQIIRDLKETQKKCLKTAGLEQKVQ 122
QY 127 KAEMLCTLKKOMKFLQRODETKQAREEAHRLCKKAKTMQIELLQSQSEVEEMIRQ 186
Db 123 KKDPLISSYVEQIGVLKSDAHVVDGLRKREKNTKLSQIQSMGISAIIAAGSADADRLKN 182
QY 187 MGVSQSAVEQIAYVCSLKEKEYENIK---EARKATGELADRLKKDLYVSR---SKLTL 239
Db 183 ----EADPHVLAMVSTLKLRELROCESKKTLELRNVKVVQNDLKRKEIELKRAYHNIPNV 238
QY 240 NTELDQAK-----LELSAQKDLQSDQETIS--LRKSSDDPGNLEPASATNETVSRLV 292
Db 239 ESDLYQAOEKLOAEKNTAYLDSPNASCGLNSILALKREERTTISP--TVKENIKR-I 295

```

```

QY 293 FESPAPVEMANRLHQPFGDEIDLNTTFDVNTPPTQSGSQHCLPKK--LCLELAR-SP 349
Db 296 EESTSPY-----LNT-----KSSVGLAHLNTKGNIGLAKSKISP 331
QY 350 MONVLLKRVHKVSKESPQSLGQRCVGELEDELAGAPLEFIRNAVLGOKOPNRTTASRS 409
Db 332 IKGVGGVSMTS-----GTIRKTSDDLSEKYSIF-----KKPRLLGSSSS 372
QY 410 STDVVRIG---FDGLGRTKFIQPRDTTIIIRVPVSKAKSKOKVRITVS 458
Db 373 SALTATGSMFNVYMGMGSEK-----VDPFAQRAEEGLSTIRSSALS 416

RESULT 9
Q9M143 PRELIMINARY; PRT; 506 AA.
ID Q9M143
AC Q9M143;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE PUTATIVE RING ZINC FINGER PROTEIN.
GN AT4G01270.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Euphorbia; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RU Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RU Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AL161491; CAB80936.1; -.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 506 AA; 56518 MW; 1B06751A4E299FE8 CRC64;

Query Match 9.2%; Score 221; DB 10; Length 506;
Best Local Similarity 21.9%; Pred. No. 0.00016;
Matches 120; Conservative 79; Mismatches 193; Indels 156; Gaps 24;

QY 5 SLCTICSD---FFDHSRDVAALHCGHTFHLOCLIQWFEFAPS---RTCPQCRIQVQKTI 57
Db 10 AICSDCYEDLKPVENNQISISA--CGHVPHFELCLOQWFEFCPSYNNKRCPCCKOKCSLKD 67
QY 58 IINKLFPDLAQEEENVL-----DAEFLKNEIDSVYKAQLSQDKREKRSQAIITDLRL 104
Db 68 PCRLYFSSGNGQDTSISDKVYGTEEDPVLLKGVYKRLKGVQVLTSLAKKKKEENVEVS 127
QY 105 DTLRDLE-----ERNATVESIQNALNKAEMLCSTLKKOMKFLQRODETKQARE 154
Db 128 DKLQCHNQDLKEDKVKRMEALQETSTQHLKLKSEBQIQNSQCVLQER--TVLAK 184
QY 155 FAHLKLC-----KMKTYEQIELLQSQ--QRSEVEEMIR--DMGV 189
Db 185 ELASIKLVSDLSLEDDVLKLLAGNNAKTDITDLYVKSIVINRSYKELACNOLGR 244
QY 190 GOS-AVQOLAYVCSLKEKEYENIKAEARKATGELADRLKKDLYVSR---SKLTL 248
Db 245 GEASSSERLEKALEIKELKRMKELELITERENRALRQINYSK---KCSYTYSEPAI 301
QY 249 ELRSQKDLQSDQETISLRKSSDDPGNLEPASATNETVSRLVESPAPVEMANRLHQP 308
Db 302 ESMSSFRLL-SSDNKV-----EKISTPGKLEKQGFITQSGCL-----RGRE 343

```

QY	309	PEPGEIDLNTTPVNV---TPPTQTSG-----SOHCPLPKKLCLEASPQNVL	354
Db	344	DSEVSRTP--SVVIDDDDYVETNTSGTRDMNTNIEEKGDNSMKDKFKFIRKIDPTSSV-	400
QY	355	KKVHVKSPEQO-----LSIGGRCVQ-----ELDEELAGAPPLIRNAVLGQK	399
Db	401	-----SPYSGSGSNIMQSSGTRNNRLNGRWSKHGERNEATPPSLGSSVP-----	441
QY	400	PNRTTAERSRSTDVYRGFDGLGRTKFIOPDRTTIIRPVVPVSKASKO-----KVRI	453
Db	442	-----RKDDLLISIGPDGKGRK-----VLRSKPOISKTNWASSGSGKRFXLGT	484
QY	454	KTVSSASQ	461
Db	485	KTSGSSSQ	492
RESULT	10		
P90990			
ID	P90990	PRELIMINARY;	PRT; 425 AA.
AC	P90990.		
DT	01-MAY-1997 (TrEMBLrel. 03, Created)		
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	B0432.9 PROTEIN.		
GN	B0432.9		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;		
OC	Rhabdilitidae; Pelioderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RY	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN-BRISTOL N2.		
RX	MEDLINE=94150718; PubMed=7906398;		
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,		
RA	Bofield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,		
RA	Craixon M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,		
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,		
RA	Jones M., Keshav J., Kirsten J., Lalster N., Latreille P.,		
RA	Lichtning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,		
RA	Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showmken R.,		
RA	Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,		
RA	Therry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,		
RA	Watson A., Weinstein L., Wilkinson-Sprout J., Wohlmann P.;		
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.		
RT	elegans.";		
RL	Nature 368:32-38(1994).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RP	STRAIN-BRISTOL N2.		
RC	STRAIN-BRISTOL N2.		
RA	Henkhaus J., Wohlmann P.;		
RT	"The sequence of C. elegans cosmid B0432.";		
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.		
RL	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BRISTOL N2;		
RA	Waterston R.;		
RL	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		
DR	EMBL; U08036; AAB37893.1; "		
DR	InterPro; IPR001841; Znf_fing.		
DR	Pfam; PF00097; zf-C3HC4; 1.		
DR	SMART; SM00184; RING; 1.		
DR	Zinc-finger.		
QO	SEQUENCE 425 AA; 48104 MW; 375F524E5C092B2D CRC64;		

Query Match 8.5%, Score 204.5; DB 5; Length 425;
 Best Local Similarity 25.9%; Pred. No. 0.001;
 Matches 73; Conservative 49; Mismatches 105; Indels 55; Gaps 12.

Db	184	PTSLIOGSCSICFEDLKNOKDKISAIYCGHIYHHCISOMLAT--KRCPCSCRTYVRKNGF	24.1
Oy	59	INKLFFDLAQ---EEENVLDAEFLAKNELDSYKAAOLSOKDREKDSQAIIDTLADTLEERN	115
Db	242	VERKLEFDVORNGGEKREKPELDYREEHY---KLSTSLVEODEKLTGTLATTEKNNLKD--	294
Oy	116	ATVESLQNAL---NKAEMLCSTLKKOMKFLERODHETKOAREEVARHLCKMKMTQEIOL	171
Db	295	---TVKSLEKKIIRKEDKYKOEIPIKQIATINHLTISEETAVLAKRELQSKARKLTCEFYKI	353
Oy	172	LLOSORSVEEMIRDMGVGSAYVQLALVYCSVLK---EYENLKEKRAKTELADRLK	227
Db	354	LTVH-----SSADQOLGEY---LKKNNIDTERTFQMLKST-----NK	389
Oy	228	DVLSRSKLTKLTLNELDOAKLELRSQAKDLOSADQETISLAK	269
Db	300	DLTKR---REAKETIDOLKNEVS---LKRRAQDEDAALTK	424

RESULT	11
Q9QZ84	
ID	Q9QZ84
AC	Q9QZ84;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2001 (EMBLrel. 17, Last annotation update)
DE	LEK1 (FRAGMENT).
GN	6530404A2Rik.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCHI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	GEOlink=99303627; PubMed=10373470;
RA	Goodwin R.L., Pabon-Pena L.M., Foster G.C., Bader D.;
RT	"The cloning and analysis of LEK1 identifies variations in the
RL	Leu-centromere protein F/mitosis gene family.";
DR	J. Biol. Chem. 274:18597-18604 (1999).
EMB	EMBL: AF194970; AAF07196.1
MD	MGD: MGI:1915046; 6530404A2Rik.
FT	NON_TER
SEQ	I I
LOC	2473 AA; 281903 MW; 504E91A1A150A3B5 CRC64;

Query Match	8.5%;	Score 204.5;	DB 11;	Length 2473;
Best Local Similarity	20.5%;	Pred. No. 0.0063;		
Matches	95;	Conservative 101;	Mismatches 163;	Indels 105;
				Gaps 14

Qy	56	KTINKLFFPLDAGEEN----	VIDAEFLIKNEIDSVAAQISQNDREKRSQAIIIDPLRQL	111
Db	1629	KOTVETLERELERKEEKEOALIDISEKLAKEVETTLAKAODEMTKSLRIFELDLVPRER	1688	
Qy	112	EEBAAVESLONALNKAEMCLSTLKKOMKFLER-----	ODETKOAREEA	156
Db	1689	ENLAKOEOEKOSRVSSELDCESSLRILREKEEQARVOMEDEKSAAMLQOMQKELAREEV	1748	
Qy	157	HLCKMKHTMOQJELLQOSRSEVEEIMIRMGSGASVQOLAVCVSLKKEVENLKEARK	216	
Db	1749	ALALONDETTLKAOQSLODQGEVEVHHH-----	KSSIKRLVYHIDADCKKQNTLEOLK	1801
Qy	217	ATYGLADRLK-----	KDLV-----SSRSKLTNTLEQAKTELRSQAOKU-	257
Db	1802	ESKHADHLKDRVENLEBOELLSEKNNMIFQAEKSKAEIOTLSEIORMQMOJODQLELI	1861	
Qy	258	-----OGAODEISLXKESDDPRGNLSPASATPEVYSR-----	LYFESAPREPMNNPLH	307
Db	1862	STRSENEMLIKELKKEOEKERSVSDLETTINPSELTLLKKEOEKAYOMKEBAITVEMLOTOIK	1921	
Qy	308	QRPGEDEIDLNTTFDVNTPPTQTSQSOHLCKPKKLCERASRPMOVLKVKHVSRSRESOL	367	
Db	1922	-----ELINEVY-----	VSICKDO-----EVSCKTQO-	1942

Db 724 QIOLEKESIEQOLAL-----KONELE-DFOKQSESEVHLQEIKAQNTQKDFELVESGES 777
Qy 104 IDTLRDTLEERNATIVESIONALNKAEMLCSTLKQKM-FLEORODETKOAREAHRLCK 162
Db 778 LKKLQOOLEQKTLGHEKIQALAE-----LKRKEKITIKKEDELOOLQSKSSES 830
Qy 163 MKTME-QIELLLQSORSEVEEMIRDMGVGQSAVEQLAVYC---VSLKREYNTL---KE 213
Db 831 LKVAVQVLEQLOQQAAGSEGSKTIVAKLHDEISQLKSOAEFTQSELKSTQSLNLEAKSKQ 890
Qy 214 ARKATGELADRLKRD-LVSSRSKIKTLNTELDQAKLELRSAQKLOKQASODEITSLRKKS 271
Db 891 LEAAGSELEEKKSCHLLEQITTKL-----SEVGERQAAISCHTQVESKTKQ----- 939
Qy 272 DDPGNTLEPASATNETVSRVLESPA-----PYEMNPNRLHQ----- 308
Db 940 -----LEAANAALAEKVAKYEASRAEASDLQDKKKEITDTLHAALQAEKSSSALHLTKL 993
Qy 309 PPGGDEI-----DLNTPFDVNTPTPTQTSQSOHCLPKKLCLEERARSPMQ----- 351
Db 994 SKFSEIATGHKELTSKAD-----AMSGEMLOKKEKLELOELRQOLODSQDSQTKLAE 1045
Qy 352 -----NYLKKVHKVSKPESQSLSGQRCVGELEDELAGAPPLIRNAVIGOK 398
Db 1046 GERKEKSEESIKNLQEEVTAKTENLELSTGTQTTIKDLERLE-----ITNLELOHK 1099
Qy 399 QPNRTTASRSSTDVYRIGFDGLGRTKFIQPRD-TTIIIRPVYKSKAKSKOKVTKTVS 457
Db 1100 -----EKMASEDAQKIA-----DLKTIVEALQVANNANISATNELSTVYL 1138
Qy 458 SASQ 461
Db 1139 EVLQ 1142

RESULT 14
Q07369 PRELIMINARY; PRT; 2139 AA.
ID Q07569
AC Q07569; 002504;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
GN MICA.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HMI:IMSS;
RX MEDLINE=93295430; PubMed=8515774;
RA Raymond-Denise A., Sansonetti P., Guillen N.;
RT "Identification and characterization of a myosin heavy chain gene
(mhca) from the human parasitic pathogen Entamoeba histolytica.";
RL Mol. Biochem. Parasitol. 59:123-131(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HMI:IMSS;
RA Guillen N.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: L03534; AAB46065.1; -.
DR HSSP: P08799; 1MND.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00242; MYSC; 1.
SQ SEQUENCE 2139 AA; 245225 MW; C68307341DB51DD1 CRC64;

Query Match 8.0%; Score 191.5; DB 5; Length 2139;

Best Local similarity 22.1%; Pred. No. 0.027;
Matches 97; Conservative 83; Mismatches 161; Indels 97; Gaps 16;
Qy 66 LAQEEENVLDAEFLKNELDVSKAQLSQK-----DREKRSQALIIDTLRTELRNATV 118
Db 1671 VAQEEEEK-----QRLSEDAIELEQLEQEDERTTAANAEAERKKIQAELEDEVKFNLEEDVTNQR 1726
Qy 119 ESL--QNALNKAEMLCSTLKQKMFLFORODETKOAREAHRLCKMKTMEQIELLLQSQ 176
Db 1727 EKLVAKNSEMDAEI--DSLKEKKALE---DEIEKITDDNNKLS-----EIDSIDKRY 1775
Qy 177 RSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLEKARKATGELADRLKRDVSSRSKL 236
Db 1776 NALLDSKSDVSMKKEKFDDELKVTKDALETEKKNHAEFTMRILKG-----FLKEEAFAEVQRL 1831
Qy 237 KTLNTELDQAKLELRSAQKLOKQASODEITSLRKSSDDPPGNTLEPASATNETVSRVLESP 296
Db 1832 EALQKNLDAQOEKARKKRAADGELKSLNNELDVKKDLDKRA----- 1876
Qy 297 APVEMNPNRLHQPPGDEIDINTTDP-----VNTPTQTSQSOHCLPKKLCLE-----R 345
Db 1877 -----QDDLADKEDELATLQDKYKTLVKKSVFDSRIQE-MQEQLDLEKAGRAK 1924
Qy 346 ARSPQNVLLKVKVSKPESQL-----SLGQRCVGELEDELAGAPPLIRNA 393
Db 1925 AOKQKQAEYKLOELQENDNDFEYKETAADRINTLSAQ--DDLQKEL-----EK 1973
Qy 394 VLQKQPNRTTAE-----SRSSDVYRIGFDGLGRTKFIQPRD-TTIIIRPVYKSKAKS 447
Db 1974 ERGLKQDSEKEVQRLRVKQCOLETKVAEVG--GANVSIKAKYKAEIEELTTEADAL 2031
Qy 448 KQVRIKTVSSASQPKLD 465
Db 2032 KAKMAEKKAKTSQKKLD 2049

RESULT 15
Q04992 PRELIMINARY; PRT; 2017 AA.
ID Q04992
AC Q04992; 024138;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE NONMUSCLE MYOSIN-II HEAVY CHAIN.
GN ZIP OR CG15792.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96144835; PubMed=8568878;
RA Mansfield S.G., al-Shirawi D.Y., Ketchum A.S., Newbern E.C.,
RA Klehart D.P.;
RT "Molecular organization and alternative splicing in zipper, the gene
that encodes the Drosophila non-muscle myosin II heavy chain.";
RL J. Mol. Biol. 255:98-109(1996).
DR EMBL: U35816; AAB09048.1; -.
DR EMBL: U35816; AAB09051.1; -.
DR HSSP: P10587; 1BR2.
DR FlyBase: FBgn0005634; zip.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_N.
DR InterPro: IPR002928; myosin_tail.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; myosin_N; 1.
DR Pfam: PF01576; myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.

DR SMART: SM00242; MYSC: 1.
DR PROSITE: PSS0096; IO: 1.
SQ SEQUENCE 2017 AA; 232089 MW; 8C76FEF2EBD02EBE CRC64;

Query Match 7.9%; Score 190; DB 5; Length 2017;

Best Local Similarity 23.8%; Pred. No. 0.03; Mismatches 145; Indels 76; Gaps 14;

Matches 88; Conservative 61; Mismatches 145; Indels 76; Gaps 14;

QY 56 KTIINKLFPDLAEEENVLDAE--FLKNELDVYKAQLSQRKREKDSQ-----AI 103
D 1263 KTVLEK-----AKGTLEAENADLATELRSVSSROENRRKQAESQIAELQVKLAE 1314
QY 104 IDTRLDTLEER-----NATVESLONLKAEMLCSTLKKQMKFLBORODETKQAREEAHR- 158
D 1315 IERRSELQEKCTKLQOEAENITNMLEEALKASAAVKSASNMESQLTEAQOLLEETRQ 1374
QY 159 ---LCKMKMTMEQIELLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKREYENLKEAR 215
D 1375 KLGLSSKLRQIESSEKALQOELDEDEKRNYY---ERKLAVITVQOMEIKKKAEDADLA 1431
QY 216 KATGELADRLKDLVSSRSKLT---NTELDQAKLELRSQKQ---LQSADEITSLR 268
D 1432 KELEGGKKRLKKDIEALERQVKELIAQNDRLDKSKKIQSELEDAITELAQRTKVELE 1491
QY 269 KKSDDPGNLEPASATNNTVSRVLFESPAPYEMNPRLOHPFGDEIDLNTTFVNPPT 328
D 1492 KKQK---NFKITLAEKAISEQIAQERDTAREAREKETVLSVSRDLDAFP----- 1541
QY 329 QTSQSQHCLPKKCLTERASPMQNVL-----KKVHKVSKP---ESQLS-LGGQ 372
D 1542 -----KIEDLENKRKTLQNELDLANTQGTADKNVHELKAKALLESQALAEKQ 1591
QY 373 RCVGELDEEL 382
D 1592 N-BELEDL 1599

RESULT 16
Q9W0W8 PRELIMINARY; PRT: 2056 AA.
AC Q9W0W8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ZIP PROTEIN.
GN ZIP OR CG15792.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pharyngota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA Burtis K.C., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abill J.F., Agbayanl A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintakov S.,
RA Borokov D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunham B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegian C.,
RA Jatali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshnell A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "the genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL: AE003465; AAF47311.1; -;
DR HSSP: P10587; IBR2.
DR Flybase: FBgn0005634; zip.
DR InterPro: IPR000048; IO.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_N.
DR InterPro: IPR002928; myosin_tail.
DR Pfam: PF00612; IO; 1.
DR Pfam: PF00063; myosin_head; 2.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR Prodom: PD000355; myosin_head; 1.
DR SMART: SM00015; IO; 1.
DR SMART: SM00242; MYSC: 1.
DR PROSITE: PSS0096; IO; 1.
SQ SEQUENCE 2056 AA; 236627 MW; 1D074D9CER1538E4 CRC64;

Query Match 7.9%; Score 190; DB 5; Length 2056;

Best Local Similarity 23.8%; Pred. No. 0.031; Mismatches 145; Indels 76; Gaps 14;

Matches 88; Conservative 61; Mismatches 145; Indels 76; Gaps 14;

QY 56 KTIINKLFPDLAEEENVLDAE--FLKNELDVYKAQLSQRKREKDSQ-----AI 103
D 1302 KTVLEK-----AKGTLEAENADLATELRSVSSROENRRKQAESQIAELQVKLAE 1353
QY 104 IDTRLDTLEER-----NATVESLONLKAEMLCSTLKKQMKFLBORODETKQAREEAHR- 158
D 1354 IERRSELQEKCTKLQOEAENITNMLEEALKASAAVKSASNMESQLTEAQOLLEETRQ 1413
QY 159 ---LCKMKMTMEQIELLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKREYENLKEAR 215
D 1414 KLGLSSKLRQIESSEKALQOELDEDEKRNYY---ERKLAVITVQOMEIKKKAEDADLA 1470
QY 216 KATGELADRLKDLVSSRSKLT---NTELDQAKLELRSQKQ---LQSADEITSLR 268
D 1471 KELEGGKKRLKKDIEALERQVKELIAQNDRLDKSKKIQSELEDAITELAQRTKVELE 1530
QY 269 KKSDDPGNLEPASATNNTVSRVLFESPAPYEMNPRLOHPFGDEIDLNTTFVNPPT 328
D 1531 KKQK---NFKITLAEKAISEQIAQERDTAREAREKETVLSVSRDLDAFP----- 1580
QY 329 QTSQSQHCLPKKCLTERASPMQNVL-----KKVHKVSKP---ESQLS-LGGQ 372
D 1581 -----KIEDLENKRKTLQNELDLANTQGTADKNVHELKAKALLESQALAEKQ 1630
QY 373 RCVGELDEEL 382
D 1631 N-BELEDL 1638

```
RESULT 17
Q94987 PRELIMINARY: PRT: 2057 AA.
ID 094987
AC 094987:
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE NONMUSCLE MYOSIN-II HEAVY CHAIN.
GN ZIP OR CG15792.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96144835; PubMed=8568878;
RA Mansfield S.G., al-Shirawi D.T., Ketchum A.S., Newbern E.C.,
RA Kiehart D.P.;
RT "Molecular organization and alternative splicing in zipper, the gene
RT that encodes the Drosophila non-muscle myosin II heavy chain.";
RL J. Mol. Biol. 255:98-109(1996).
DR EMBL: U35816; AAB09049.1; -
DR EMBL: U35816; AAB09050.1; -
DR HSSP: P10587; 1BR2.
DR Flybase: FBgn0005634; zip.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF00663; myosin_head; 2.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
SQ SEQUENCE 2057 AA; 236642 MW; 0D59519C1E83A411 CRC64;
```

```
Query Match 7.9%; Score 190; DB 5; Length 2057;
Best Local Similarity 23.8%; Pred. No. 0.031;
Matches 88; Conservative 61; Mismatches 145; Indels 76; Gaps 14;

QY 56 KTIINKLFFDLQAEENVLDAE--FLKNELDYKQAQLSQKREKDSQ-----AI 103
DB 1303 KTVLEK-----AKGTLEAMADLATELRSVNSRQENDRRRRKQASQIAELQVLA 1354
QY 104 IDTLRDITLEER-----NATESIQNALNKAEMLCSFLKQMKFLEORODETKQAREEHR- 158
DB 1355 IERRASELQEKCTKIQQAENITNLEAEELKASAAVKSASMSQSLTEAQLLEETRQ 1414
QY 159 ---LCKMKTKTEQLELLIQSORSEVEEMIRDMGVGQSAVEQLAVVCSLKEYEENLKEAR 215
DB 1415 KLGSSTKLRQIETSEKEALQOELEEDDEAKRMY---ERKLAETVQMQEIKKAEEDADA 1471
QY 216 KATGELADRLKDKDVSSSKTKTL--NTELDQAKLELRSAQKDL--LQSADEQITSLR 268
DB 1472 KELEGGKRLKKDIEALERQVKELAONDRLDKSKKKIQSELEQDTIELEQRTKVELE 1531
QY 269 KKSDDPPGNLEPASATNETVSRLEFESPAPVEMMNPRLHQPPFGDEIDLNTFFDVNTPPT 328
DB 1532 KKQK---NPKILAEKAISEQIAQERDTPAREAREKETVLSVSRLEDAFD----- 1581
QY 329 QTSQSQCPLPKKCLERRASPMQNVL-----KKVHKVSKP-----ESQIS-LGGQ 372
DB 1582 -----KIEDLENNKRTLQNELDLDLANTQGTAGKNVHELEKAKRALSSQLAELKAQ 1631
QY 373 RCVGELDEEL 382
DB 1632 N-BELEDDL 1639
```

```
RESULT 18
Q9QYT2 PRELIMINARY: PRT: 1447 AA.
ID 09QYT2
AC 09QYT2:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 16, Last annotation update)
DE MEA2/GOLGA3 PROTEIN.
GN MEA2/GOLGA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL6;
RA Matsukuma S.;
RT "Mea2/Golga3 Gene Product is Indispensable for Spermatogenesis in the
RT Mouse.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB029537; BAA86880.2; -
DR EMBL: AB029521; BAA86880.2; JOINED.
DR EMBL: AB029522; BAA86880.2; JOINED.
DR EMBL: AB029523; BAA86880.2; JOINED.
DR EMBL: AB029524; BAA86880.2; JOINED.
DR EMBL: AB029525; BAA86880.2; JOINED.
DR EMBL: AB029526; BAA86880.2; JOINED.
DR EMBL: AB029527; BAA86880.2; JOINED.
DR EMBL: AB029528; BAA86880.2; JOINED.
DR EMBL: AB029529; BAA86880.2; JOINED.
DR EMBL: AB029530; BAA86880.2; JOINED.
DR EMBL: AB029531; BAA86880.2; JOINED.
DR EMBL: AB029532; BAA86880.2; JOINED.
DR EMBL: AB029533; BAA86880.2; JOINED.
DR EMBL: AB029534; BAA86880.2; JOINED.
DR EMBL: AB029535; BAA86880.2; JOINED.
DR EMBL: AB029536; BAA86880.2; JOINED.
SQ SEQUENCE 1447 AA; 162776 MW; 53087BE7460B3B6F CRC64;
```

```
Query Match 7.9%; Score 189.5; DB 11; Length 1447;
Best Local Similarity 22.7%; Pred. No. 0.023;
Matches 95; Conservative 77; Mismatches 158; Indels 89; Gaps 16;

QY 65 DLADBEENVLDA-EFLKNE-----LDYKQAQLSQKREKR-----DSQAITITLRD 109
DB 712 ELQREADSDREDAIHFQNEKIVLEVALQSAKSDKEELDRCARLEEDTETSGLEQLRQ 771
QY 110 TLEERNATVESIQNALNKAEMLCSFLKQMKFLEORODETKQAREEHR-RODET-----KQ 151
DB 772 DLAYSKNOVEHLQOE-----TATLRKQKQVKVEQFVQLGVVWEAARRDQTSQDLQNE 824
QY 152 AREEABRLCKMKTKMEQLELLIQSORSEVE-----EMIRDMGVGQSAVEQLAVVCSLKE 207
DB 825 LKATVKRLRDSMKELRQELIKLOGEKKTVEVEHSHRLQKMSLVHQQMAELGHLQSVQKE 884
QY 208 YEN-----LKEA-----RKATGELADRLKDKDVSSSKTKTLTMTELDQA 246
DB 885 RDEMEIHLQSLKPFKEQMIATLEANKETLKQIEELOQBAKKAITEQKKMRRLSDLSLA 944
QY 247 KLEIRSAQKQDSQDOETSLRKKSDDPPGNLEPASATNETVSRLEFESPAPVEMMNPRL 306
DB 945 QKEKTKTKKATVENA---VSIISRQEA---LASKKATDAELNOLRAOSTG---GSSDVL 996
QY 307 HQPPFGDEIDLNTT-----FDVNTPTPTQTSQS-QHCLPKKCLERRASPMQNVLKKV 357
DB 997 HEKIRALEVELQNVGQSKILLEKELOEVIYITMTSQDELESRRKVLLEBDELOESGFRKI 1056
QY 358 HKVSKPESQSLSGQRCVGVGELDEELAGAPFLFIRNAVIGQKQKPNRTTAESRSSSTDVRI 416
DB 1057 KRLSESNKRLAL-----ELEHERGKLTGIGQSNAAALREHNSILLETALAKREADIVQL 1108
```


OC Eukaryota; Lobosea; Gymnamoebia; Amoebidae; Amoeba.
 OX NCBI_TaxID=5775;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D.
 RX MEDLINE=99082369; PubMed=9864850;
 RA Oh S.W., Jeon K.W.;
 RT "Characterization of myosin heavy chain and its gene in Amoeba
 proteus".
 RL J. Eukaryot. Microbiol. 45:600-605(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D;
 RA Oh S.W., Jeon K.W.;
 RL Submitted (Mar-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF136571.1; AAD33718.1;
 DR HSP; P08799; IAMD.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; Myosin_N.
 DR Pfam: PF00612; IQ; 2.
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR PRODOM: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 SQ SEQUENCE 2138 AA; 244427 MW; DB58B308639FA71 CRC64;

Query Match 7.9%; Score 188.5; DB 5; Length 2138;
 Best Local Similarity 22.2%; Pred. No. 0.039;
 Matches 102; Conservative 69; Mismatches 170; Indels 119; Gaps 17;

QY 56 KTIINKLFFDLAQBENVLDAFLKNEIDSVKAQISQ----- 92
 DB 1247 KRLVAKLESDKKMKKEVEDERDLKNKLDIAQK-KLSQAELDELGNALBEMAKNRSREKN 1305
 QY 93 -KDREKR-----DSQAIIITDL-----RDTLEERNATVESLONALNKAEMLCSTL 135
 DB 1306 RKDLENRLRELEDOAEDEQAARSNLEKFRGFEDNLEHOSQVDEVODVAVLSAAKKL 1365
 QY 136 KKQMKLEFORODETKQAREEAHRLCKMKKME---QIELLQSORSEVEEMIRMGVGO 191
 DB 1366 ESELEAKRSLDNEAEGRKVAEE---KKKVLDTLHELQIALSNANKNTGLVRNVKVVQ 1422
 QY 192 SAVQGLAVVYCVSLKKEYENLKEARKATGELADRLKKDLYSSRSKLTINTELDOAKELR 251
 DB 1423 DEVEDLNEQYEMASKELSKLDKGNKKTAELEKELRRHYQESQS-----SLDAGELKLR 1475
 QY 252 SAQKDLSADOEITSLRKKS-----DDPGNLEPASATNETVSRILVFESPA 297
 DB 1476 HTQDELDLHMQLEDLEKSSLSRSKKQLOLOYDDLEDTHEELAAATKAEKRLVKDLEA 1535
 QY 298 PV-EMANRHLQPPGCD-----EIDL-----NTTF-----DV 323
 DB 1536 DIALEQETRVSEFPLMAQEKALSLLEVELVLDLKKDADROSAFAKVENERSALREYBDL 1595
 QY 324 NTPPTQTS---GSGHCLPKKL-----CLERARSPMONVLLKVVHVSFPESQLSIGG 371
 DB 1596 QAOQDETSTKLANADRAKKLINTLDQSLKLEKASNAQKSLERKLKKAERDLAAAKAAS 1655
 QY 372 QRCVGL-DEEL--AGAFPLFIRNAVIGQKOPNRTTAESR 408
 DB 1656 ARAGGVSDELRRQAQAEALALRDA--DREKSNKLTIAEKR 1694

RESULT 22
 ID 028714 PRELIMINARY; PRT: 1156 AA.
 AC 028714;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CHROMOSOME SEGREGATION PROTEIN (SMC1).
 GN AFI558.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
 OC Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrtides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sultion G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glöck A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus".
 RL Nature 390:364-370(1997).
 DR EMBL: AE000995; AAB89690.1;
 DR TIGR: AFI558;
 DR InterPro: IPR003439; ABC_transportr.
 DR InterPro: IPR003405; SMC_C.
 DR InterPro: IPR003395; SMC_N.
 DR InterPro: IPR02017; Spectrin.
 DR Pfam: PF02483; SMC_C; 1.
 DR Pfam: PF02463; SMC_N; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 1156 AA; 134244 MW; 18CB16F7CD5AD1ED CRC64;

Query Match 7.8%; Score 186.5; DB 17; Length 1156;
 Best Local Similarity 16.7%; Pred. No. 0.026;
 Matches 76; Conservative 111; Mismatches 152; Indels 125; Gaps 13;

QY 55 KTIINKLFFDLAQBENVL-----DAEFLKNE----- 82
 DB 671 KERMISDKIVELQREKEGLFAELNRAESLRQYQDEVORLTGMISELNRISLDEKIRT 730
 QY 83 -----LDSKADLSQDKRK-----RDSQAIIITDLRDTLEERNATVESLONALNKAEML 131
 DB 731 ESGRIEELREKISQSRKENYISLKDYNKSLAEMEAIGLEIAEIERMLRGSE-- 788
 QY 132 CSTLKKQMKFLEORODETKQAREEAHRLCKMKKT---EQIELLQSQ-----RSEV 180
 DB 789 ---VPKIVIEEDKIKEEQRNRRELLISTEKKIESIEFRREOLBESSMOEKQYIDEIKDRI 845
 QY 181 EEMIRDMGVQSAVQALAVVYCVSLKKEYENLKEARKATGELADRLKKDLYSSRSKLTN 240
 DB 846 DEIRRTIEEGKARVVEINSELEIRKEBERELGELGKLRERDELQOLRNAEKEKKIE 905
 QY 241 TELDQAKIELRSADQDSADOEITSLRKSDDPGNIPEPASATNETVSRILVFESPAVE 300
 DB 906 AEIRLERIRIQLQERELEIAESEAIGEV--EVPENLPLEKVEKYLDELV----- 955
 QY 301 MMNRLHQPFGDELDINTFTDVMTPTQ-----TSGSGHCLPKKLCLERARSPMONVLLK 355
 DB 956 -----VELSTFGDVNLKALQIEYEAVKARDELVEKMYLEKERA--DILD 998
 QY 356 KVRHVSFPESQLSIGQRCVGLDELDLQAEPLFIRNAVIGQKOPNRTTAESSTDVVR 415
 DB 999 RIEKYEKMKREI-----FEVE-----TAINRFAELIR 1027
 QY 416 IGFDGLGRKFIQPRDTTIIIRPVVSKAKSKOKVRIRKIVSSASQ 461
 DB 1028 ---ELANGEGELYLDSDDPFNSGLYIKVYKPNKPVQKLSKSGEK 1070

```

RESULT 23
ID 026079 PRELIMINARY: PRT: 1941 AA.
AC Q26079;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Placopecton magellanicus (Sea scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
OC Pectinoidea; Pectinidae; Placopecten.
OX NCBI_TaxID=6577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKELETAL MUSCLE;
RA Perrault-Micale C., Kalabokis V., Milyray L., Szent-Gyorgyi A.G.;
RT "Sequence variations in the surface loop near the nucleotide binding
RT site modulate the ATP turnover rates of molluscan myosins.";
RL J. Muscle Res. Cell Motil. 0:0-0(1996).
DR EMBL: U59294; AAB03660.1; -.
DR HSSP: P24733; IMDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS00096; IQ; 1.
SQ SEQUENCE 1941 AA; 223243 MW; E2AD1637FFDB8127 CRC64;

Query Match 7.7%; Score 184; DB 5; Length 1941;
Best Local Similarity 22.4%; Pred. No. 0.061;
Matches 97; Conservative 71; Mismatches 131; Indels 134; Gaps 19;

QY 55 KRIITIKLPFD--LAQEEENVLDAEFLKNELDSVK-----AQLSQ 92
DB 906 EKLIQKADPESSQIKLEERLDEDAASDLGSIKKMEGDANLNKKDIGELEHSLQKSE 965
QY 93 KDKERDSQAIIIDL-----RDTLEERN-ATVESLQ-----NALNKA 128
DB 966 QEKAKHDNQ--ISTLOGESQDDEHIGLKNKEKKALEFNAKKTSDSLQAEEDKCNHLNK- 1022
QY 129 EMLCSTLKQMKFLEORODETKQAREEAHRLKCKMK-----TMEQIELLLQSQRSEVEEM 183
DB 1023 --LKAKLEQLDELDELDEREKVKRGDVEKAKSKVEDLKSQENVEDLERVKR-EELEN 1079
QY 184 IR-----DMGVGSAVQLAVYCVSLKKEVENLKEAKKATGELADRLKDLVSS 232
DB 1080 VRKKEAEITTLNSKLDEQNLVSQLRKIKELQARIEELEELAEERNASVKEKQRAEL 1139
QY 233 RSKIKTLNTELDOA-----KLELSAQKDLQSA-----DOETISLRKKSDDP 274
DB 1140 NRELEELGEHLDEAGATSAQIQLNKKREAEELKIRDLDEASQIQAQSAIRKKKQD- 1198
QY 275 PGNLEPASATNETVSRLVFESPAVEMMNPRLHQPFGDEIDLNTTFDVNTPTQTSGSQ 334
DB 1199 -----AANEMADQV-----DOLQKVKSLKLEK-----DKDKLREMD-----DLESQMT 1236
QY 335 HCLPKKLCLEARRSPMGNVLKKNHVKSPESQSLSGQRCVGELEDELAGAFPLFINNAV 394
DB 1237 HDKNNKGSCKSVKQKQFES-----QVSDLNARLE-DSQRSINEL----- 1273
QY 395 LGOKOPNRRTAES 407

```

```

DB 1274 --QSKSRLOAEN 1284
RESULT 24
ID 091BD4 PRELIMINARY: PRT: 1937 AA.
AC 091BD4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=HEART;
RX MEDLINE=20149854; PubMed=10684978;
RA Machida S., Noda S., Fututani Y., Takao A., Momma K., Matsuoka R.;
RT "Complete sequence and characterization of chick ventricular myosin
RT heavy chain in the developing atria.";
RL Biochim. Biophys. Acta 1490:333-341(2000).
DR EMBL: AB032197; BAA92710.1; -.
DR HSSP: P08799; 1MND.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRINTS: PR00194; TROPOMYOSIN.
DR PRODOM: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
SQ SEQUENCE 1937 AA; 223473 MW; 95A94F69CDB36781 CRC64;

Query Match 7.7%; Score 183.5; DB 13; Length 1937;
Best Local Similarity 20.4%; Pred. No. 0.065;
Matches 78; Conservative 81; Mismatches 165; Indels 59; Gaps 11;

QY 59 INKLFPLDQEEENVL--DAEFLKNEIDSVKAOISQKDKERDSQAIIIDRLDLEERNA 116
DB 1267 MTRLMNDLTQTKRKLOSENGEFVR-QLEKESLSIQSRKSTSTFTQIIEELRRQLEDEETK 1325
QY 117 TVESLONALNKAMLCSTLKQMKFLEORODETKQAREEAHRLKCKMKKTMEQIELLLQSQ 176
DB 1326 SKNALHAALQAAHDDCDLLLEQYEEEOEAKAELORALSKNAEVAQWRTYETDAIORTE 1385
QY 177 RSEVEEMIRMGV-----GQSAVEQLAVYCVSLKKEVENLK-----EARKATGELADR 224
DB 1386 --ELEDKAKKLAARLOEAEEAITEANAKGSLKTYHRLQNELEDMMIDLEKNSAASL 1443
QY 225 LKRDVSSRSKLTLN--TELDOAKLELSAQKDLQSAQDOETISLRKKSDDPPGNLEPA 281
DB 1444 DKK-----QRFEDKIINDWKMKYEQSAQLEASQKEARSLSLTELFLKLNVAEETLDHETL 1499
QY 282 SATNETVSRLVFESPAVEMMNPRLHQPFGDEIDLNTTFDVNTPTQTSGSQHCLPKKL 341
DB 1500 KRENKNLQEEIISDLTNOISGNKNLH-----ETL-----KVKKQVEQEKSEVOL 1543
QY 342 CLRARRSPMGNVLKKNHVKSPESQSLSGQRCVGELEDELAGAFPLFINNAVIGOKOPN 401
DB 1544 ALDEAGALHEHSKTLRFOLELSQLKADPERKLAEDQEMENI-----RRNQ 1592
QY 402 RT-----TAESRSSTDVARI 416

```

Db 1593 RTIDSLDSTDEARSREAIRL.1615

RESULT 25

Q9NJ23

ID Q9NJ23

AC Q9NJ23

DT 01-OCT-2000

DT 01-OCT-2000

DT 01-DEC-2001

DE MOSIN HEAVY CHAIN STRIATED MUSCLE SPECIFIC ISOFORM (FRAGMENT).

GN MHC.

OS Aequipecten irradians (Bay scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;

OC Pectinoidea; Pectinidae; Argopecten.

OX NCBI_TaxId=31199;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20090924; PubMed=10623517;

RA Yamada A., Yoshio M., Ojwa K., Nyltray L.;

RT "catchin, a novel protein in molluscan catch muscles, is produced by

RT alternative splicing from the myosin heavy chain gene.";

RL J. Mol. Biol. 295:169-178(2000).

DR EMBL: AF183909; AAF62391.1; -.

DR HSSP: P24733; IWDG.

DR InterPro: IPR000048; IQ.

DR InterPro: IPR001609; myosin_head.

DR InterPro: IPR002928; Myosin_tail.

DR InterPro: IPR002017; Spectrin.

DR InterPro: IPR000533; Tropomyosin.

DR Pfam: PF00612; IQ; 2.

DR Pfam: PF01576; myosin_head; 1.

DR Pfam: PF01576; myosin_tail; 1.

DR PRINTS: PR00194; TROPOMYOSIN.

DR PRODOM: PD000355; myosin_head; 1.

DR SMART: SM00015; IQ; 1.

DR PROSITE: PSS0096; IQ; 1.

DR NON_TER 1

FT 1

SQ SEQUENCE 1219 AA; 141202 MW; BAC6F574DA4AFBBB CRC64;

Query Match

Best Local Similarity 7.6%; Score 183; DB 5; Length 1219;

Matches 102; Conservative 67; Mismatches 128; Indels 146; Gaps 20;

Db 55 KKTINKLPD-----LAOEENVLDAEFLKNEIDSVKADL-----SQ 92

Db 184 EKLMQKADDESQIKLEERLDEEDAAADLEGITKKMEADNANLKKDIDGENTLOKAE 243

QY 93 KDKRKDSQALIDTL-----RDTLEERN-AVESIQ-----NALNKA 128

Db 244 QDKAHKNO--ISFLQGEISQDEHIGKLNKKKALEANNTKTSIDLAEDKCNHLNK- 300

QY 129 EMLCSTKKQKFLQKQKDEKQKAREAHNLKCKMK-----TMDQIELLQSORSEVEM 183

Db 301 --LKAKLEQALDELEDEMLERKKYKRGVDEKAKKRVEDOLKSTQENVEDLEKVR-EELEN 357

QY 184 IR-----DMVGQSAVEQOLAVYCVSLKKEVENLKARAKATGELARLKKDLVSS 232

Db 358 VRKKEAFISSNKLDEQDQNLVSQLRKIKELQRIELEELEELAEARNARAKVKKQRAEL 417

QY 233 RSKIKLNTLTDQA-----KLELRSAOKDQSA-----DOEITSLRKKSDP 274

Db 418 NRELEELGERLDEAGATSAQIELNKKREAEKLLKIRDLERASQIHQKQISALKKKHOD- 476

QY 275 PGNLEPASATNETVSRVLFESPAPVEMNPRLOPPFGDEIDLTTFDVTPTQTSQSO 334

Db 477 -----AANEMADQV-----DQLQKVKSKLEK-----DKKDLKREMD-----DLESQMT 514

QY 335 HCLPKKICLERARSPMONVLKKVHKVSKPESQLS-----LGGRCVGELDEELAGAPPL 388

Db 515 HNMKNKGCSEK-----VMKQF-----BSQMSDLNARLEDSQRSINEL----- 551

QY 389 FIRNAVLCQKOPNRTTAESRSST 411

Db 552 -----QSOKSRLOAENSIDL 566

RESULT 26

Q9NCL3

ID Q9NCL3

AC Q9NCL3

DT 01-OCT-2000

DT 01-DEC-2001

DE MUD PROTEIN.

GN MUD.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxId=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20345122; PubMed=10884435;

RA Guan Z., Prado A., Melzig J., Heisenberg M., Nash H.A., Raabe T.;

RT "Mushroom body defect, a gene involved in the control of neuroblast

RT proliferation in Drosophila, encodes a coiled-coil protein.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:8122-8127(2000).

DR [2]

RP SEQUENCE FROM N.A.

RA Prado A., Raabe T.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF209068; AAF89163.2; -.

DR FlyBase: FBgn0002873; mud.

DR SEQUENCE 1871 AA; 216126 MW; AE3BE89F9937F76D CRC64;

Query Match

Best Local Similarity 7.6%; Score 181.5; DB 5; Length 1871;

Matches 79; Conservative 69; Mismatches 144; Indels 67; Gaps 11;

QY 56 KTTI---NKLFDLAOGEEVND--AEFLKNEIDSVKQKQSD-----REK 97

Db 1243 KSVIEAQTQKSDLDQKREKESAOQLVDNLKVELDKERKELQVNSAFQKTSDDLQREK 1302

QY 98 RDSQAIIIDTLRDLTEENRATVESLQNALNKAKEMCTFLKQKFLQKQKDEKQKAREAH 157

Db 1303 ESAQQLVDNLKVELDKERKELAQVKSIVIAQTKLSDDLQKESAOQLVDNLK- 1356

QY 158 RIKCKMKTQEIQLLQSORSEVEEMIRDMVGQSAVEQOLAVYCVSLKKEVENLKARAKA 217

Db 1357 ELDKERKELAKVKSIVIAQTKLSDDLQKESAOQLVDNLKVELDKERKELAQVNSAFEA 1416

QY 218 TGEIADLKLKDLVSSRSKLTNTLQDAKIELRSADKQDQSAQDEITSLRKKSDPPGN 277

Db 1417 QTKLSDDLQKESAOQLVDNLKVELDKER-----KELAQVSAIGAQTKLSDD- 1465

QY 278 LEPASATNETVSRVLFESPAPVEMNPRLOPPFGDEIDLTTFDVTPTQTSQSOHL 337

Db 1466 ---LEQKESVQQLVDNLKVELDKERELAK-----VNSAFEAQTK-----L 1504

QY 338 PKKICLERARSPMONVLKKVHKV--SKPESQLSG-----GRCVGELEDELAGAF 386

Db 1505 SDDLKQKEDAQREVFLVKERLVKEKREFVKLATLDTIETLEMRCQ--QMEERARAV 1562

RESULT 27

Q9EON8

ID Q9EON8

AC Q9EON8

DT 01-MAR-2001

DT 01-MAR-2001

DT 01-JUN-2001

DE MITOSIN (FRAGMENT).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Qian M., Lin D., Zhu X.;
 RT "Evolution of the internal repeat of mtosin."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF182407; AAC06839.1;
 DR InterPro: IPR000533; Tropomyosin.
 DR PRINTS; PRO0194; TROPOMTOSIN.
 FT NON_TER 1 324
 FT 324
 SQ SEQUENCE 324 AA; 37896 MW; A6ACD5A55EIDFD7D CRC64;

Query Match 7.6%; Score 181; DB 11; Length 324;
 Best Local Similarity 21.4%; Pred. No. 0.014;
 Matches 65; Conservative 75; Mismatches 106; Indels 58; Gaps 9;

QY 56 KTIINKLFFLAQEEEN---VLDAEFLKNEIDSVKAOISQDKREKRSQAIIIDTLRDTL 111
 Db 25 KDVVENLERLEMSSEKQELALIDSENLKAEVETLKAQMDMAKSLRVFELDLVNVRSER 84
 QY 112 EERNATVESLQNALNKAEMLCSTLKQKMFLEQRODETKQAREBAHR-----LKCKM 163
 Db 85 ENLAKQOEKQSVSELDLCSLR-----SLSEKEQARVQWEMDSKSAIMLITQTL 137
 QY 164 KTM-EQIELL-----LOSREVEEMIRMGVQSAVEOLAYCVSLKE---YENLK 212
 Db 138 KEMVEEVAALYNDOETLKAQEOSIDQGEVHLKSSIQRLKVAHIDAKKKCHILEQLK 197
 QY 213 EARKATGELADRL-----KKDLV---SSRSKLTNTNLELDQAKLELSAOK 255
 Db 198 ESHHMDLEKRVENLEFOELMLSEKNEHLIPQENSKAEIQTLTETIQMDNLQDEL 257
 QY 256 DLQADQELTSLRKSDDPGNLEPASATNETVSRLV-----FESPAPVEMNP 304
 Db 258 ELNTREREKLNMLKELKNEQDISKLETTINSIERLLKDKQEKVQVKEARITVENLQT 317
 QY 305 RLHQ 308
 Db 318 OLKE 321

RESULT 28
 066878 PRELIMINARY; PRT; 1156 AA.
 AC 066878;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CHROMOSOME ASSEMBLY PROTEIN HOMOLOG.
 GN XCPG OR AQ_629.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 RN NCBI_TaxID=63363;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-VF5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus."
 RL Nature 392:353-358(1998).
 DR EMBL: AE000699; AAC06839.1;
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR InterPro: IPR003716; RNA_pol_omega.
 DR InterPro: IPR003405; SMC_C.
 DR InterPro: IPR003395; SMC_N.

DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF02483; SMC_C; 1.
 DR Pfam: PF02463; SMC_N; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 1156 AA; 135563 MW; B12DB30F70C0CEA9 CRC64;

Query Match 7.6%; Score 181; DB 16; Length 1156;
 Best Local Similarity 20.1%; Pred. No. 0.051;
 Matches 81; Conservative 92; Mismatches 141; Indels 88; Gaps 16;

QY 66 LAQEEENV---LDAEFLKNEIDSVKAOISQDKREKRSQAIIID---TLRDLERNATVE 119
 Db 207 LKEKEKLEKFKELQRTKRETA-KILKKEKELKRERLINLSSRESLEIDTQIQ 265
 QY 120 SLONALNKAEMLCSTLKQK-----KLEQRODETKQAREBAHRLCKMKMTQOIEL 171
 Db 266 ENEKELERERLLKEVNEKIMPEKEVGKFTAEIENERSIKEREKESENVKMLEE 325
 QY 172 LLOSREVEEMIRMGVQSAVEOLAYCVSLKKEVENLKEARKATGELADRLKDLVS 231
 Db 326 LNNLSDKENLEREVGTTQLELEK-----LKEETKSLKEV----- 361
 QY 232 SRSKLTNTNLELDQAKL---ELRSQKDLQADQELTSLRKSDDPGNLEPASATN--- 285
 Db 362 EREKRLRELEEEERLKTTPPEVKLEEEKKELTKELSLNKKOEL---ELQNALNKKIE 419
 QY 286 ---ETVSRLVESPAPV-----EMNPRLHQPEGEIDL-NTTPVNPPTQSSQH 335
 Db 420 RIKEDINKLISEREKIKEIKKEQOETIKRLKAIRKKEEELRNLTQLEINYEKR----- 473
 QY 336 CLPKKLLEARSMQVNLKVNHVSKPESOLISGGRQCEGLDELAGAPPLFIRNAV 395
 Db 474 -----LSEVRKKLEVELEKGAIEREVSFS-----DVSDVKRDKGVGSV-SLI 519
 QY 396 GOKOPNRTAESRSTDVVRIGFDLGRTRKFIQPRDTIIR 437
 Db 520 RVKNPEHITA-----IEVAG-GGRLEKFIYVEDEYAK 550

RESULT 29
 090337 PRELIMINARY; PRT; 1933 AA.
 AC 090337;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinus.
 RN NCBI_TaxID=7962;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-FAST SKELETAL MUSCLE;
 RX MEDLINE=97352533; PubMed=9208928;
 RA Hirayama Y., Watabe S.;
 RT "Structural differences in the crossbridge head of temperature-
 RT associated myosin subfragment-1 isoforms from carp fast skeletal
 RT muscle."
 RL Eur. J. Biochem. 246:380-387(1997).
 RN [2]
 RN SEQUENCE OF 738-1933 FROM N.A.
 RC TISSUE-FAST SKELETAL MUSCLE;
 RX MEDLINE=97176447; PubMed=9023993;
 RA Imai J., Hirayama Y., Kikuchi K., Kakimura M., Watabe S.;
 RT "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
 RT muscle and their gene expression associated with temperature
 RT acclimation."
 RL J. Exp. Biol. 200:27-34(1997).
 DR EMBL: D89990; BAA22067.1; -

DR EMBL: D50474; BAA09067.1; -
 DR HSSP: P13538; 2MYS.
 DR InterPro: IPR000048; IO.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; myosin_N.
 DR InterPro: IPR002928; myosin_tail.
 DR Pfam: PF00612; IO; 1.
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF02736; myosin_N; 1.
 DR Pfam: PF01576; myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IO; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PSS0096; IO; 1.
 KW Myosin.
 SQ SEQUENCE 1933 AA; 221092 MW; CDF0CBAA475530F5 CRC64;

Query Match 7.6%; Score 181; DB 13; Length 1933;
 Best Local Similarity 19.9%; Pred. No. 0.088;
 Matches 99; Conservative 91; Mismatches 170; Indels 138; Gaps 18;

QY 31 LQCLIQMFETAPSRTPCPCRIQVGKTIINKLFEDLAQEEENVLD----AEFLKNELDS 85
 DB 1142 LEETISERLEEAGATAQIEKNKKREAFQKMRDL---EESTLQHEATAALRRKKQADS 1198
 QY 86 VKAQLSOK-----DREKDSQAIITLADTLEERNAYESLONALNKKEMLCST 134
 DB 1199 V-ALGEOIDNLQRIKOKLEKESEYKMEIDL-----SSNMEAVKAKGNLEKMCRT 1250
 QY 135 LKKOMKPLEORODETKQAREAHRLCKMKT-----MEOIELL----- 172
 DB 1251 LEDDLSEIKAKSDENSRYLNMNARARLQTENGEFSQLEKEKALYSQLTRGQAFTQ 1310
 QY 173 LOSORSEVEEMIRMGVQSAVEQLAVYCVSLKREYENLKAR-----KATGELAD- 223
 DB 1311 IEDLKRHYEEEVAKNALAHAVQSAHRHDCDLLRQYEEQAKAKELQNGMSKANSEVAK 1370
 QY 224 -----RLKDDVSSRSKLTNTNE---LQAKLELSAOKD--- 257
 DB 1371 RAKETDAIOTTELEESKKKLAQRLQDAEESIEVNSKASLETQKRLQSEVEDLMD 1430
 QY 258 -----QSADQETILSKKSDDPGNLEPASATNFTSVLVEESPAPVE-- 300
 DB 1431 GERANALANLDKQKQNRNDKVLADMKQYEEQAELQAQKAEARSLSLELFKMNSTYEA 1490
 QY 301 -----MANPRLHQPPFGDEIDLNTTFDVNTPPTQSGSCHLPK-----K 340
 DB 1491 LDHLETLKREKNLQO-----EIS-----DLSEQLGETGKSIHELEKAKTVESEKAEIQ 1540
 QY 341 LCLERARSPMONVLKRYHKVSKPESQSLSGQRCVGEDELDELAAFLFTINA--VLGQK 398
 DB 1541 TALEEAGCTLEHESKTLRQLELNOVKSETIDRLAEKDEEM---DQIKNSQRLVDSM 1596
 QY 399 QPNRTAESRSSIDYVRI 416
 DB 1597 Q-STLSEVRSRNDALRV 1613
 RESULT 30
 Q9UT73 PRELIMINARY; PRT; 1940 AA.
 AC 09UT73;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 OS Pecten maximus (King scallop) (Pylarim's clam).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Periomorpha; Pectinoidea;
 OC Pectinoidea; Pectinidae; Pecten.
 OX NCBI_taxid=6579;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=ADDUCTOR MUSCLE;
 RA James D.P., Patel H., Chantler P.D.
 RT "Primary structure of myosin from the striated adductor muscle of the
 ATLANTIC scallop, Pecten maximus."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF134172; AAD52842.1; -
 DR HSSP: P24733; IMDC.
 DR InterPro: IPR000048; IO.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; myosin_N.
 DR InterPro: IPR002928; myosin_tail.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00612; IO; 2.
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF02736; myosin_N; 1.
 DR Pfam: PF01576; myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IO; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PSS0096; IO; 1.
 SQ SEQUENCE 1940 AA; 223141 MW; A3D09DECBEB16F90 CRC64;

Query Match 7.6%; Score 181; DB 5; Length 1940;
 Best Local Similarity 23.0%; Pred. No. 0.088;
 Matches 101; Conservative 67; Mismatches 125; Indels 146; Gaps 20;

QY 55 KTIYINKLFED--LAQEEENVLDAEFLKNELDSYK-----AQLSQ 92
 DB 906 EKLIMQKADFESQIKLELEERLDEDAADLEGIKKMETQNSLKKDIDGLENTIQAE 965
 QY 93 KDRKDSQAIITPL-----RPTLEERN-ATYESIQ-----NALNKA 128
 DB 966 QDKAHKDNQ--ISTLOGEMAQDEHIGIKLNKKKALEANKKTSLSQAEEDKCNHLNK- 1022
 QY 129 EMLCSTLKKOMKPLEORODETKQAREAHRLCKMK-----TMOIELLQSORSEVEEM 183
 DB 1023 --LAAKLEQALDELEDNLERKKKRGVDEKAKKRVBDLKTQENVEDLEVKR-ELLEN 1079
 QY 184 IR-----DMGVQSAVEQLAVYCVSLKREYENLKARKATGELADRLKDDVSS 232
 DB 1080 VRKREAEISTLNSKLEDBQNLVSOQRKVKELQRIEELBELAEARNARAKVEKQRAEL 1139
 QY 233 RSKRLTNTLEDOA-----KLELSAOKDLQSA---DOETLSLKKSDDP 274
 DB 1140 NRELLEELGERLDEAGATSAQIELNKKREAEELKIRRLDEASLQHEAOISALRKKHD- 1198
 QY 275 PGNLEPASATNETVSRILVFESPAPVEMNPRLHQPPGDEIDLNTTFDVNTPPTQSGSQ 334
 DB 1199 -----ANEMADQV-----DQIQVKSYLEK---DKDKIREND-----DLESQMT 1236
 QY 335 HCLPCKLCLERARSPMONVLKRYHKVSKPESQSL--LGGORCVGEDELDELAAFLPL 388
 DB 1237 HNMKNKGCSK-----YMKQF-----ESQMSDLNARLDSQRSINEL----- 1273
 QY 389 FIRNAVLGQKQPNRTAES 407
 DB 1274 -----QSQKSRLOAEN 1284

RESULT 31
 Q02015 PRELIMINARY; PRT; 2007 AA.
 AC 002015;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE NONMUSCLE MYOSIN HEAVY CHAIN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
 OX NCBI_TaxId=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92388144; PubMed=1355479;
 RA Takahashi M., Kawamoto S., Adelstein R.S.;
 RT "Evidence for inserted sequences in the head region of nonmuscle
 myosin specific to the nervous system. Cloning of the cDNA encoding
 the myosin heavy chain-B isoform of vertebrate nonmuscle myosin.";
 RL J. Biol. Chem. 267:17864-17871(1992).
 DR EMBL: M93676; AAA48987.1; -
 DR EMBL: M93676; AAA48986.1; -
 DR EMBL: M93676; AAA48985.1; -
 DR EMBL: M93676; AAA48988.1; -
 DR HSSP: P10587; 1BR2.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00612; IQ; 1.
 DR Pfam: PF00663; myosin_head; 2.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50096; IQ; 1.
 DR PROSITE: PS50096; IQ; 1.
 SQ SEQUENCE 2007 AA; 232592 MW; 36A591368CD264BA CRC64;

Query Match 7.64; Score 181; DB 13; Length 2007;
 Best Local Similarity 21.58; Pred. No. 0.091;
 Matches 96; Conservative 87; Mismatches 167; Indels 96; Gaps 16;
 OY 68 QEEENVLDIAEFLKNEIDSVKASQKREKRDQAIIIDTLDEERNATVESIQNALNK 127
 DB 1536 QNKRLADMELMSSKDVGNVHLEKSKR-----TLEQVEMTQLELEDELQA 1588
 OY 128 AEMLCSTLKQMKFLERODETQAREBAHRLCKM-KTMEQIELLIQSQRSE----- 179.
 DB 1589 TEDAKLRLVMMQAKKQAFERDLOARDEONEKKRMVLVQVRELEAELEDERKORALAVA 1648
 OY 180 -----VEEMIRMGVGO-----SAVEOLAVYCVSLKREYMKERKRTGTGLADRLK 226
 DB 1649 AKKMEHMDLQD-EGQLEANKARDEATKQRLQAQMKDYORELEEARARDEIFPAQSK 1707
 OY 227 KDLYSSRSKLTNTLTEDQAKLELSAQKDSADOETISLRKSDDPGNNLEPASATNE 286
 DB 1708 E-----SEKTLKGLAEITLQOEFAASERARHHAQDEHDEL--ADELIANSASGKSALLD 1760
 OY 287 TVSL-----VESPAVPMANRHLHQPFGDEIDINTTFVDVNTPTPTQTSGSGHC 336
 DB 1761 EKRLLEARIQLEBELEEEOSNMELNERFRK-----TTLQVDTNLSELAGERSA 1810
 OY 337 LPKLCLEERASPMQNVLYKVH-KVSKPESQSLSGQKCVGELDELAGAPPLIRNAVVL 395
 DB 1811 AQKS-----ENARQOLERONKELAKLOLEGSVKSKFKATISTLEKTIQOL----- 1857
 OY 396 GQKQPNRTTASRSSTDVIRIGFDLGGRTK-----FIQPRD-----TTIIRPVVSKSA 445
 DB 1858 -EEGLEDEAKRAANAKLV-----RTEKKIKVEYMWQVEDERHNDQYKKEQMEKXANA 1908
 OY 446 KSKQKVR-----IKYVSSASQPKL 464
 DB 1909 RMKQLKROLEAEAEATRANASRRKL 1934

RESULT 32
 ID 096720 PRELIMINARY; PRT; 692 AA.
 AC 096720;

DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PARAMOSTIN-LIKE ALLEGEN (FRAGMENT).
 OS Dermatophagoides farinae (House-dust mite).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Acariformes; Sarcopitiformes; Astigmata; Analgoidea; Pyroglyphidae;
 OC Dermatophagoides.
 OX NCBI_TaxId=6954;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98389068; PubMed=9723675;
 RA Tsai L.C., Chao P.L., Shen H.D., Tang R.B., Chang T.C., Chang Z.N.,
 RA Hung M.W., Lee B.L., Chua K.Y.;
 RT "Isolation and characterization of a novel 98-kd Dermatophagoides
 farinae mite allergen.";
 RL J. Allergy Clin. Immunol. 102:295-303(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20062524; PubMed=10594536;
 RA Tsai L., Sun Y., Chao P., Ng H., Hung M., Hsieh K., Liaw S., Chua K.;
 RT "Sequence analysis and expression of a cDNA clone encoding a 98-kDa
 allergen in Dermatophagoides farinae.";
 RL Clin. Exp. Allergy 29:1606-1613(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Tsai L.-C., Chao P.-L., Ng H.-P., Chua K.-Y.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF352244; AAK39511.1; -
 FT NON_TER 692
 FT 692
 SQ SEQUENCE 692 AA; 81372 MW; 61FC6380C9D7C9E2 CRC64;

Query Match 7.58; Score 180; DB 5; Length 692;
 Best Local Similarity 21.98; Pred. No. 0.034;
 Matches 87; Conservative 64; Mismatches 160; Indels 86; Gaps 13;
 OY 59 INKLEFPDIAEENVL--DAEFLKNEIDSVKASQKREKRDQAIIIDTLDEERNNA 116
 DB 104 INRVIELTSHKQRLSQENTELIK-EVHEVQLQDNNANHLKTQIAQOLETRHLEEEER 162
 OY 117 TVESIQNALNKAEMLCSTLKQMKFLERODETQAREBAHRLCKM-KTMEQIEL 171
 DB 163 KRASIDENAHITLVELELSKQVL-----DESEARLELRQTLKANGDAASMSKYEYA 215
 OY 172 LLQSORSEVEEMIDMGV-----QSAVQOLAVYCVSLKREYENK-----EARRATG 219
 DB 216 ELQAHAEVEELRRKMAQKISEYEEOLEALLNKCSLEKQSRLOSEVEVLIIMLEKATR 275
 OY 220 ELAD-----RLKDIVSSRSKLTNTLTEDQAKLELSAQKDSADOETISLRKSD 273
 DB 276 HAQOLEKRVADLEKINDLKKLEEVYIMLQDAQKELRYKIAEIQKLOHEKRLDQDQ 335
 OY 274 PPGNLEPASATNETVSRVSPAPVEMMNRLHQPFGDEIDINTTFVDVNTPTPTQSGS 333
 DB 336 -----LARENKLTDLDAKSQLNDARRHE-----QELIEIKR----- 370
 OY 371 QHCLPKLCLEERASPMQNVLYKVH-KVSKPESQSLSGQKCVGELDELAGAPPLIRNAVVL 379
 DB 371 -----LENERDELSAAYKAEETLKKQEVAN--QRLTIAELAVRHDYERKLAKD 418
 OY 418 ELAGAPPLIRNAVILGQKPNRTTASRSSTDVIR 416
 DB 419 EIEELRKQY--QTEIEQLNMRLAEAEKKTETIARL 453

RESULT 33
 ID 021440 PRELIMINARY; PRT; 1992 AA.
 AC 021440;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)


```

Db 1410 ALETAGSKCLHDTKNOILQOEILLSMKTQVKCKEKLQKNK-----KLBOEVL 1458
OY 384 GAFFLIRNAV-LGOKOPNTTAESRSSTDVVRIGFDGLGRTKFIOP-----R 431
Db 1459 NLRSHIERNNVELGQYKQYQOEIEERAROEIA-----EKLKVNLFLQAOAASQENLEQFR 1514
OY 432 DTTIIRPVYKSAKSKQVRIKTSS 458
Db 1515 ENNE-----ASMSQOMELRIKDLES 1534

RESULT 35
O9H1Q1 PRELIMINARY; PRT: 1710 AA.
ID 09H1Q1
AC 09H1Q1
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE BAL45E8.1 (KIMA1074).
GN BAL45E8.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162272; CAC19649.1;
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS0297; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1710 AA; 196410 MW; 01CBF9BADB894872 CRC64;

Query Match 7.5%; Score 179.5; DB 4; Length 1710;
Best Local Similarity 19.2%; Pred. No. 0.093;
Matches 109; Conservative 111; Mismatches 182; Indels 165; Gaps 22;

OY 16 HSRDVAIHCGHTFHLLQCLQWETAPSRTPQC-RIOVGKTTINKLFFDLAQEEN-- 72
Db 1010 HSRDLAAIH--DRDQSTSRLELAFQARDCSRQ-----DKMNDVSNLKNNE 1060
OY 73 -----VDAEFLKNELDVYKALOSKREKRDSQA 102
Db 1061 ILSQOLFETESKLSLEIEFHHTDALREKTLGIERVQKDLSTOCOMEKQYQOEY 1120
OY 103 IIDTL--RDTLEERNATVES-----LQNLNKA-----EMLGS 133
Db 1121 KVKVYIGKQSVBERLSQLOSEMMLRQOLDDAHNRKADNEKTYINIQDFHAIYQKLA 1180
OY 134 TLKQMFLEQRODETQAREEAHRLCKMKMTM-----QTELLLOSQSEVEEMIRDMGV 189
Db 1181 ESKQSLLEER--NKEILSECNHLKERQYQYENENKAKEBEVYVROQLQDLATLKQSM 1237
OY 190 GQSAVEQLAVYCVSLKEYENLKAARKAGELADRL-----KKDL 229
Db 1238 SEASLEVTSTRYRILEDOTDLK---KILQIRNOLEADRHTEAVRCAEKKMDHROKL 1294
OY 230 VSASRSLK-LTLNTELDQAKLELSAQKDLQSD-----OEITSLRKSSDPPGNLEPAS 282
Db 1295 EKQNAKLKTVKQMD---KIEBLQNLNLNANLSEDEKQLKMLKLOSLECNLDQEM 1350
OY 283 ATNEVSRILVFESPAVEEMNPRLOHPFGD-----EID-----LNTTFDVT 325
Db 1351 KKNVLEIREITGFKLLKMKRKRLNEVENGEFPHDGLKTSQFEMDIQIKLKHIDLT 1410
OY 326 PRPQTSQ--HCLPKKLCLEARSPQONVLLKVVHYSKSPQSLSLGGQRCVGLDELA 383
Db 1411 ALETAGSKCLHDTKNOILQOEILLSMKTQVKCKEKLQKNK-----KLBOEVL 1459

```

```

OY 384 GAFFLIRNAV-LGOKOPNTTAESRSSTDVVRIGFDGLGRTKFIOP-----R 431
Db 1460 NLRSHIERNNVELGQYKQYQOEIEERAROEIA-----EKLKVNLFLQAOAASQENLEQFR 1515
OY 432 DTTIIRPVYKSAKSKQVRIKTSS 458
Db 1516 ENNE-----ASMSQOMELRIKDLES 1535

RESULT 36
O90338 PRELIMINARY; PRT: 1092 AA.
ID O90338
AC O90338;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN (FRAGMENT).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxId=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-FAST MUSCLE;
RX MEDLINE-97176447; PubMed-9023993;
RA Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
RT "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
RT muscle and their gene expression associated with temperature
RT acclimation."
RL J. Exp. Biol. 200; 27-34(1997).
DR EMBL; D50475; BA09068.1;
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON TER 1
SQ SEQUENCE 1092 AA; 125885 MW; B6BABA3963BEEBA CRC64;

Query Match 7.5%; Score 179; DB 13; Length 1092;
Best Local Similarity 17.7%; Pred. No. 0.062;
Matches 89; Conservative 94; Mismatches 172; Indels 148; Gaps 13;

OY 31 LQCLQWETAPSRTPQCRIQYGKTTINKLFFDLAQEENVLDAEF----- 78
Db 302 LEEISERLEEGAGATAQIEMNRKREADFOKMRDL---BESTLOHEATAALRKQADT 358
OY 79 ---LKNELDVYKALOSKREKRDSQAIIDTLRDTLEERNATVESLQNALNKAMELCS 135
Db 359 VAELEGQIDMLQYKQKLEKESEYKMEIDL-----TSNMEYAKAKGNLEKMRIL 411
OY 136 KQKMFLEQRODETQAREEAHRLCKMKMT-----MEQIEL-----L 173
Db 412 EDLSEIKAKSDNSRQNLNMNQRARLQTEENGEFNSQLBEKALYSQLTRGQAFTQI 471
OY 174 QSORSEVEEMIRDMGVQSAVEQLAVYCVSLKEYENLKAAR-----KATGELA--- 222
Db 472 EDLQRHVEEYKAKNALAHVQSAHRDCDLRQYEEQDEAKTELQSGMSKANSEVAQWR 531
OY 223 -----DRLKDL-----VSSR----- 233
Db 532 AKYETDAIORTLELEPAKKKLAORLDAESISAVSSKASLEKTORLOGEVEDLMDIG 591
OY 234 -----SKLTLNTELDQAKLELSAQKDLQSDADEITSLRKKSDPP 275
Db 592 ERANANLQKQRFNDKVLAEWKQANAKYEESSQALEAQAQEARSLSTELFKMNSYEAL 651
OY 276 GNLEPASATNEVSRILVFESPAVEEMNPRLOHPFGEDLNTTFDVTNPRPQTSQSOH 335
Db 652 DHELTREKRNKNLQOEISLSEQLGETGKSIHELEKAKKIVSEKAEIQF----- 701

```

QY 336 CLPRLKLERARSPMGNVLKVKHVKSPESQSLSGGRCVGEDELDELACGAPFLIFIRNA-- 393
 Db 702 -----ALFEAESEHLEHEESKILFVQLQELNQVKEIDRKLAENKEEL-----EQIKRNSQR 751
 QY 394 VLGGKOPNRTTAESRSTDVYRI 416
 Db 752 VMSMQ-STLDEIRSRNDALRV 773

RESULT 37

Q26080 PRELIMINARY; PRT; 1950 AA.
 AC Q26080;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 OS Placopecten magellanicus (Sea scallop).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 OC Pectinoidea; Pectinidae; Placopecten.
 OX NCBI_Taxid=6577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ADDUCTOR MUSCLE;
 RA Pterault-Micale, C, Kalabokis V., Nyitrai, L, Szent-Gyorgyi A.G.;
 RT "Sequence variations in the surface loop near the nucleotide binding
 RT site modulate the ATP turnover rates of molluscan myosins.";
 RL J. Muscle Res. Cell Motil. 0:0-0(1996).
 DR EMBL: U59295; AAB03661.1; -.
 DR HSSP: P24733; 1WDC.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00612; IQ; 2.
 DR Pfam: PF00663; myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50096; IQ; 1.
 SQ SEQUENCE 1950 AA; 224184 MW; 6FE358802352C19A CRC64;

Query Match 7.5%; Score 179; DB 5; Length 1950;

Best Local Similarity 21.9%; Pred. No. 0.11;
 Matches 95; Conservative 70; Mismatches 134; Indels 134; Gaps 18;

QY 55 KTIITINKLFDP--LAOEENVLDAEFLKNELDSYK-----AQLSQ 92
 Db 905 EKLMQKADFESEIKLEELKRLDEBDAASDLEGKKKMECDNANLKKDIGELSHSLQKSE 964
 QY 93 KDBEKRDQAIIIDL-----RDLEERN-AVESIQ-----NALNKA 128
 Db 965 OEKAHKDNG--ISTLQEMSGQDEHIGLKNKKKALEEANKKTSDSIQADEDKCNHLNK- 1021
 QY 129 EMLCSLTKKQMKFLQRODETKQAREAHRLKCKMK-----TMEQIILLQSORSEVEEM 183
 Db 1022 --EKAKLEQALDELEDELLEKEKRYGVDEKAKSVEDDLKSTQENVEDLERVKR-ELEEN 1078
 QY 184 IR-----DMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSS 232
 Db 1079 VRKKEAEITTLNSKLEDEQNLVLSOLOKRIKELQRIELELEAEERNASVKVQKQAEI 1138
 QY 233 RSKLKTNLTELQDA-----KLELNSAQKDLQSA-----DOETISLRKSSDP 274
 Db 1139 NRELEELGERLDEGAGTSAQIELNKKRAEALIKIRRDLEASIQHQAQISAIIRKKQD- 1197
 QY 275 PGNLEPASATNEVSRLVFSPAPVEMMNRLLHOPFGDEIDLNTTFDVNTPPTQISGSG 334

Db 1198 -----AANEMADQV--DQLQVKKSKSEKNNKMESENEDDLQAI-----Q 1235
 QY 335 HCLPRLKLERARSPMGNVLKVKHVKSPESQSLSGGRCVGEDELDELACGAPFLIFIRNAV 394
 Db 1236 HISKNGKCSSEKVMKQFES-----QVSDLNARLE-DSQRSINEL----- 1272
 QY 395 LGQKOPNRTTAES 407
 Db 1273 --QSKSRLOAEN 1283

RESULT 38

Q9BWC0 PRELIMINARY; PRT; 471 AA.
 AC Q9BWC0;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HYPOTHETICAL 54.6 KDA PROTEIN (FRAGMENT).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EYE, RETINOBLASTOMA;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC000280; AAH00280.1; -.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR000533; Tropomyosin.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00194; TROPOMYOSIN.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 471 AA; 54589 MW; 82F1E4B83BE2E135 CRC64;

Query Match 7.5%; Score 178.5; DB 4; Length 471;

Best Local Similarity 22.0%; Pred. No. 0.027;
 Matches 75; Conservative 75; Mismatches 136; Indels 55; Gaps 10;

QY 75 DAEFLKNELDSYKVAQLSQDKREKRDQAIIIDLRTLEERNATVESIQNALNKAEMLCST 134
 Db 7 DMEDLSSKXDQVGNVHELEKSKRALQGVEMKQTQLELEDELQALNEADKRLREVMQA 66
 QY 135 LKKQMKFLQRODE-----TKQAREAHRLKCKMK-----TMEQIILLQSOR 178
 Db 67 MKAQFERDLQTRDEQNEKKRLLIKQVRELEAELEDEKQORALAVASKKMEIDLKLEA 126
 QY 179 EVE--EMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSSKL 236
 Db 127 QIEANKARD-----EYIKDLKRLQAOQMDYORELEARSRDLEIFQSKK-----SEKIL 177
 QY 237 KTIINTELQAKLELRSQAQKLSAQDSQADITSLRKSSDPNPLLEPASATNEVSR- 291
 Db 178 KSLAEELIQLEELASSERARRHAQDEGDEL---ADEITNSASGSKSLDEKRLERLARIA 234
 QY 292 -----VFESPAPVEMMNRLLHOPFGDEIDLNTTFDVNTPPTQISGSGHCLPK---KLC 342
 Db 235 QLEEELEEEQSNMELLNDRRK-----TTLQVDTINAEILAEARSAAQSDNARQ 284
 QY 343 LERARSPMGNVLKVKHVKSPESQSLSG--QRCVGEDEL 382
 Db 285 LERONKELKAKLOLEBGAVSKFRKATISALEAKIGOLEOL 325

RESULT 39

Q63731 PRELIMINARY; PRT; 1999 AA.
 AC Q63731;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE NEURONAL MYOSIN HEAVY CHAIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=101116;
 RP [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE=92235856; PubMed=1569576;
 RA Sun W., Chantler P.D.;
 RT "Cloning of the cDNA encoding a neuronal myosin heavy chain from
 RT mammalian brain and its differential expression within the central
 RT nervous system[see comments]."
 RL J Mol. Biol. 324:1185-1193(1992).
 DR HSP; P10587; 1BR2.
 DR InterPro: IPR000048; IQ.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00612; IQ; 1.
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 2.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR PRODOM: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50096; IQ; 1.
 KM Myosin.
 SQ SEQUENCE 1999 AA; 231456 MW; 090C181D55727B41 CRC64;

Query Match 7.58; Score 178.5; DB 11; Length 1999;
 Best Local Similarity 20.98; Pred. No. 0.12;
 Matches 93; Conservative 81; Mismatches 153; Indels 117; Gaps 15;

QY 48 QCRVGVCKTTINLFDLQAEENV-----LDNEF--LNKELDSVKAQLSOK 93
 DB 1072 ELKMOALAKE--EELQALALAVEEBAOKNALKKIRELSQISELDLDESRRSRKA 129
 QY 94 DREKRSQALIDLTLDLTLEERNATVESIQNALNKRAEMLCSTLKK-----OMKFLDQ 144
 DB 1130 EKQRDGELEELAKTELEDITDSTAQOGLRSKREDEVNLTKEKTLBEAKTHQAQIDEM 1169
 QY 145 RQETKQAREFAHL--KCKMKTME-----QIELLOS-----QRSEV 180
 DB 1190 RQKSOAVEELAEQLEOTKRRKANLEKAKQTLNENRGELANEVKYLQGRDSEHKRRKY 1249
 QY 181 EEMIRDMGV-----GQSAVEQLAVYCVSLKKEYNLEKERRKATGELADRLKDYSSRKL 236
 DB 1250 EAQQLQELQVKNESGERRTTELADVTKLQVELDVTGLLSQSDSKSKLTDFSALESQ 1309
 QY 237 K-----TINTELQAKLELRSQKDLQASADQ-----TISL 267
 DB 1310 QDTQELQDEENRQKLSLSTKQVDEDEKNSFREQLSEEEBAKHNLEKQITLHAQVADM 1369
 QY 268 RKKSDDPPGNLEPASATN-----ETVSRLLVFESPA--PVEKMPRLHOPFGDEIDL 317
 DB 1370 KKKMEDSVGCLETAEEVVRKLOKDLGLSQRHEEKVAAYDKLEKTKRKLQDELDDLVDL 1429
 QY 318 N-----TTPDVNTPPYQTSQSHQCLRKKLCLSEKARSMQVNLKKVHKVSPPE 364
 DB 1430 DHQROSACNLEKKQKPEF-----QLAAEITTKSAKYAEERARDAEERAEKATKELSLAR 1483
 QY 365 SOLSLGQRC-----VGEIDDEL 382
 DB 1484 AELEMEKKAFLRKNLOEMTERL 1507

RESULT 40
 Q9VDZ1

ID Q9VDZ1 PRELIMINARY; PRT; 482 AA.
 AC Q9VDZ1;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE CG5555 PROTEIN.
 GN CG5555.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP [1]
 RC SEQUENCE FROM N.A.
 RC SRRAIN-BRKLEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Adayani A., An H.-J., Andrews-Plankkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cateu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
 RA De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ideyang C.,
 RA Jajal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liao X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazotto M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheefel F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1. SIMILARITY: COMTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AF003725; AAF55646.1;
 DR FLYBase; FBgn0038686; CG5555.
 DR InterPro: IPR002017; Spectrin.
 DR InterPro: IPR001607; zf-UBP.
 DR InterPro: IPR001841; znf_fing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR Pfam: PF02148; zf-UBP; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00290; znf-UBP; 1.
 KW Zinc-finger.
 SQ SEQUENCE 482 AA; 54620 MW; 89A9D9DA5CDEF39F CRC64;

Query Match 7.48; Score 178; DB 5; Length 482;
 Best Local Similarity 20.08; Pred. No. 0.03;
 Matches 74; Conservative 56; Mismatches 96; Indels 144; Gaps 14;
 QY 4 LSICTGSDPFDHSRD-VAAIHGHTFHLOCLIQWFETAPSRTPCR----- 50

```

Db 172 LPTCPVCLERHDESVGVLTILCNHAFHASCIMKMGDS-----TCPVCRHVQTPGLVEDSV 227
QY 51 -----IQVCKRTI-----INK 61
Db 228 CMECEGTSLMICLICGHVGGGRYOGGHAHAHFRATNHTFAMQIGTSSVWDYAGDNFVHR 287
QY 62 LFFDLAOREENVLDAEFLEKNEIDSVKAOISQKREKRDQAIIIDTLRDITLEERNATVESL 121
Db 288 LF-----QKSDGKLV-----ASQTEKD-----EREKIDSM 314
QY 122 QNALNKAEMLCSTLKKQKFLBQRODETKQA---REBAHRLKCKMKTMEQIELLOSQR 177
Db 315 Q-MEFTYLTLSQLDTORRYEERMERLEOEQONHKATANDAKTEVSELOOQNMQKEX 372
QY 178 SEVEEMINDMGVGSVAVOLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSRSKLK 237
Db 373 VNLE-----RKLQHTAKLKDVOQOLNEER---ELSKALQSNQSSWHGKX 415
QY 238 TLNTELDOAKLELRSQKDLQSADEITSLRKKSDD-----PGNLEPASATNETV 288
Db 416 LLEQOYNFEK-----QTHDAEYTELKQDLRDIMFPLDNQOKLANTELAGS---TV 462
QY 289 SRLVFESPAP 298
Db 463 TGIKEKEDP 472

```

Search completed: September 4, 2002, 16:15:58
 Job time: 1482 sec